

6358 AGTIAGTITITIATIAAATIGGTICAAGGTICTAACCCAAGTITAGTTTGTTTCCATGCTCGGTATAG

6418 ACTITINATITCAAATIIGGTATCGCCAAAACCAAGAAGGAACTCCCATCCTCAAAGGTTTGTA

TGAAATAAGTTTAACCATAGCGGTTTTGGTTCTTCCTTGAGGGTAGGAGTTTCCAAACAT

6478 AGGAAGAATTCTCAGTCCAAAGCCTCAACAAGGTCAGGGTACAGAGTCTCCAAACCATTA

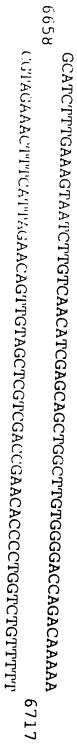
TOCTTOAAGAGTOAGGTTTCGGAGTTGTTCCAGTCOATGTCTAGAGGTTTGGTAAT

8659 CATGCATCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGG 6657

GTACGTAGTACCAGTCATTCAAAGTCTTTTTCTGTAGGTGGCTTCTGAATTTTCAATCACC

Figure

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AUGAATGGTGCAGAATTTGTTAGGCGCACCTACCAAAAGCATCTTTGCCTTTATTGCAAAG

TCCTTACCACGTCTTAACAATCCGCGTGGATGGTTTTCGTAGAAACGGAAATAACGTTTCC

ATAAAGCAGATTCCTCTAGTACAAGTGGGGAACAAAATAACGTGGAAAAAGAGCTGTCCTG

TATTTCGTCTAAGGAGATCATGTTCACCCCTTGTTTATTGCACCCTTTTTCTCGACAGGAC

TIGTICGGGTIGAGTIGATITIACGCATACTGCTTGCGTCACTGCTGGTGTTTTCTTAAGGGAGAT ACAGCCCACTCACTAATGCGTATGACGAACGCAGTGACGACCACAAAAGAATTCCCTCTA

6898 TATAAGAAGGCATTCATTCCCATTTGAAGGATCATCAGATACTAACCAATATTTCTC

ATATTCTTCCGTAAGTAAGGGTAAACTTCCTAGTAGTCTATGATTGGTTATAAAGAG

6954

Figure 1

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DIFFICURE LETTER

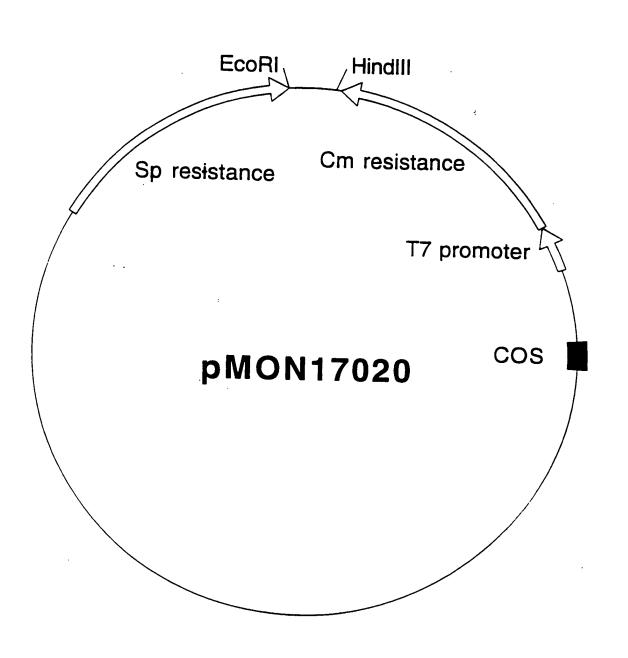


Figure 2

346	GAT Asp 95	CTC Leu	CCG Pro	GCG Ala	GAG Glu	CCT Pro 90	GCG Ala	CTG Leu	CTC Leu	GGC Gly	85 85	AAT' Asn	GGC Gly	G'FC Val	GGC G] y	GAT Asp 80
298	ATC Ile	ATC Ile	TGG Trp	ACC Thr	GAC Asp 75	GGC Gly	GAA Glu	AAG Lys	CGT Arg	ATC Ile 70	AGG Arg	GCC Ala	•. 4[5 355	ATG Met	GCC Ala 65	CAG Gln
250	ATG Met	GCC Ala	AAG Lys	GGC Gly 60	ACG Thr	AAT Asn	ATC Ile	GTC Val	GAC Asp 55	GAG Glu	GGC Gly	GAA Glu	CTG Leu	CT"F	GGC G1y	ACC Thr
202	ATC Ile	CGC Arg	ACG Thr 45	GAA Glu	GGT Gly	AGC Ser	GCG Ala	CTC Leu 40	GGT Gly	GGC Gly	Phe	ATG Met	Phe 35	TCC Ser	Arg	CAC His
154	TCC Ser	ATC Ile 30	TCG Ser	AAG Lys	GAC Asp	GGC Gly	CCC Pro 25	ATT Ile) CGC	GTC Val	ACC	GGA Gly 20	CTT TCC	Leu Leu	63y	TCT Ser
106	TCC Ser 15	AAA TC	CGC AF Arg Ly	GCC Co Ala A:	ACC G	GCA A Ala T 10	CCC G Pro A	CGG C Arg P	AGC C	AGC F	GCA A Ala S 5	Gly !	CAC (His (TCG (Ser F	ATG TMET S	
60	GGAAGACGCC	3GAA(AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA	GAT	CGTG	GAGC	G GA	30000	CTCC	360 0	TCC	TCTO	3CGT	CCCC	ÁA

ACG (Thr V	GTG Val	AAG I,ys 160	GTG Val	CGC Arg	GTC Val	Phe
GTC Val	AAG Lys	ACG Thr	AAA Lys 145	CCG Pro	TAC Tyr	61 <i>7</i>
ATC Ile	TCC Ser	CCG Pro	TCG Ser	ATG Met 130	GAT Asp	AA'I' Asn
GAG Glu 195	GCC GTG Ala Val 180	ACG Thr	GAA Glu	GGC Gly	TTC Phe 115	'GCC Ala
CCG		CCG Pro	GAC Asp	CGC Arg	GAC Asp	GCC Ala 100
ATC Ile	Leu	ATC Tle 165	GGT Gly	GTG Val	AGC Ser	ACG Thr
ATG Met	CTC Leu	ACC Thr	GAC Asp 150	TTG	ACC Thr	GGC Gly
ACG Thr	GCC Ala	TAC Tyr	CGT Arg	AAC Asn 135	TTC	TGC
CGC Arg 200	GGC Gly	CGC Arg	CTT Leu	CCG Pro	ATC Ile 120	Arg
GAT Āsp	CTC Leu 185	GTG Val	CCC Pro	CTG Leu	GGC Gly	CTG Leu 105
CAT His	AAC Asn	CCG Pro 170	GTT Val	CGC Arg	GAC Asp	ACC
ACG Thr	ACG Thr	ATG Met	ACC Thr 155	GAA Glu	GCC Ala	ATG Met
GAA Glu	CCC Pro	GCC Ala	TTG Leu	ATG Met 140	TCG Ser	GGC Gly
AAG Lys 205	GGC Gly	TCC	CGC Arg	GGC Gly	CTC Leu 125	CTC Leu
ATG Met	ATC Ile 190	GCA Ala	GGG Gly	GTG Val	ACA Thr	GTC Val 110
CTG Leu	ACG Thr	CAG Gln 175	CCG	CAG Gln	AAG	Gly
682	634	586	538	490	442	394

CTG Leu	ATC Ile	CCC Pro	CTG	GAC Asp 240	CGC Arg	CAG Gln
CGC Arg 305	GAA Glu	ACC Thr	CTT	GTG Val	ACC Thr 225	1 G]y
GTT Val	GTC Val 290	CGC Arg	GTT Val	CCG	ATC Ile	TTT Phe 210
CGC Arg	ATC Ile	ACC Thr 275	CCG Pro	GGC Gly	CGC Arg	GGC Gly
TCC Ser	AAC Asn	GGC G1y	GGC G1y 260	GAC Asp	CTG Len	GCC Ala
TCC Ser	CCG Pro	CTC Leu	TCC Ser	CCG Pro 245	GAA Glu	AAC Asn
ACG Thr 310	CGC Arg	ATC Ile	GAC Asp	TCC Ser	GGC Gly 230	C'I'I Leu
CTG Leu	CTT Leu 295	CTG Leu	GTC Val	TCG Ser	CGC Arg	ACC Thr 215
AAG Lys	GCC Ala	ACG Thr 280	ACC Thr	ACG Thr	GGC Gly	GTC Val
GGC Gly	GGC Gly	CTG Leu	ATC Ile 265	GCC Ala	AAG Lys	GAG Glu
GTC Val	GGC Gly	CAG Gln	CTC Leu	TTC Phe 250	CTC	ACG Thr
ACG Thr 315	GAA Glu	GAA Glu	AAC Asn	CCG Pro	ACC Thr 235	GAT Asp
GTG Val	GAC Asp 300	ATG Met	GTG Val	CTG Leu	GGC Gly	GCG Ala 220
CCG Pro	GTG Val	GGC G1y 285	CTG Leu	GTT Val	CAA Gln	GAC Asp
GAA Glu	GCG Ala	GCC Ala	ATG Met 270	GCG Ala	GTC Val	GGC Gly
GAC Asp	GAC Asp	GAC Asp	AAC Asn	GCC Ala 255	ATC Ile	GTG Val
1018	970	922	874	826	778	730

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GTG Val	ACC Thr 400	CGC Arg	AAT Asn	GTC Val	GCC Ala	CGC Arg 320
TCG Ser	CAT	CCT Pro 385	GGC Gly	AAG Lys) TYPC 1 Phe	GCG Ala
GAA Glu	CTC Leu	GAC Asp	GTG Val 370	GAA Glu	GCG Ala) CCT
AAC Asn	GA ? Asp	GGC Gly	GAT Asp	AGC Ser 355	GAA Glu	TCG Ser
CCT Pro 420	CAC His	AAG Lys	TGC Cys	GAC Asp	GGG G1y 340	Met
GTC Val	CGC Arg 405	GGG Gly	GAT Asp	Arg	GCG Ala	325
ACG Thr	ATC Ile	CTC Leu 390	GAG Glu	CTC	ACC	GAC Asp
GTG Val	GCC Ala	GGC Gly	GGC Gly 375	TCG Ser	GTG Val	GAA Glu
GAC Asp	ATG Met	AAC Asn	GAG Glu	GCC Ala 360	ATG Met	TAT Tyr
GAT Asp 425	AGC Ser	GCC Ala	ACG Thr	GTC Val	AAC Asn 345	Pro
GCC Ala	TTC Phe 410	TCG Ser	TCG Ser	GCC Ala	GGT Gly	ATT Ile 330
ACG Thr	CTC Leu	GGC G1y 395	CTC Leu	AAT Asn	CTG	CTC
ATG Met	GTC Val	GCC Ala	GTC Val 380	GGC Gly	GAA Glu	GCT Ala
ATC Ile	ATG Met	GCC Ala	GTG Val	CTC Leu 365	GAA Glu	GTC Val
GCC Ala 430	GGC Gly	GTC Val	CGC Arg	AAG Lys	CTC Leu 350	GCC Ala
ACG Thr	CTC Leu 415	GCC Ala	GGC Gly	CTC	CGC Arg	GCC Ala 335
1354	1306	1258	1210	1162	1114	1066

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1982	TEGGTCGGGC GGACAGTCCT TFGAAGCCCG CCGACGATGC GCACTT	TGGGTCGGGC GGAC
1936	GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA	GCGGGTTGGC CGAT
1876	GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAATG	A'I'G'I'CACCGC GT'CA
1816	TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAGCTCT	
1756	GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TGCGGCGCGT GAGCCGGGCA	
1696	ACCGGTCGGT GCTGTCGGCC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC	ACCGGTCGGT GCT
1636	CGCTTGATGA CGAGGCGCTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG	CGCTTGATGA CGA
1576	ATCTCUATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT	ATCTCGATAC GGG
1516	CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTCATC	CCGCTGCGGC
1456	TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC Ser Asp Thr Lys Ala Ala 450	GAA CTC TCC G Glu Leu Ser As 450
1402	AG TYPC APPG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC lu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile 445	AGC TYPC CCG GAG Ser Phe Pro Glu 435

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Gly GGC Ala (JCA GAC Asp Thr ACC SÁrI AAG GCC TCC. Ser Arg CGC Arg CGC Ile ATC TCG Ser TCG Ser CAT His Glu GAG Arg CGC Ala GCA Ser TCC Leu CTC Thr Phe TTC ACG Gly 20 Met ATG GGC Glu LLT, GAA Phe Gly GGC Ile ATC Gly GGT Arg CGC Leu CTC ATT Ile GCA CCG Pro 208 160

Ser TCG Gly GGC Glu GAA Thr ACC Arg CGC Ile ATC Thr ACC Gly GGC Leu CTT 50 CTGLeu Glu GAA Gly GGC Glu GAG Asp GAC Val GTC Ile ATC 256

40

Asn AÆ'l' Thr AC'A Gly GGC Arg CGCAla GCC Met A'I'G Gln CAG Ala GCC 65 Met ATG Gly GGC GCG Ala Lys AAA Ile ATC Arg CGT AAA Lys Glu GAG

Gly GGC Asp GAT 75 Val GTC Trp.,Ile TGG ATC I]e A'I'C Asn AAC Gly GGC Val GTC Gly GGC Asn AAT Gly GGC Cys TGC Leu CTG Leu TTG Gln CAG

352

304

Figure 4

AAC Asn	CCG Pro 170	CTG Len	CGC Arg	G&C Asp	ACC Thr	ecc Pro 90
ACG Thr	ATG Met	ACG Thr 155	GAA Glu	: GCC Ala	Met	C GAA 5 Glu 0
CCG Pro	GCC Ala	CTG Len	ATG Met 140	TCG Ser	GGC Gly	4 GCT 1 Ala
GGC Gly	TCC.	ATC Tle	GGC Gly	CTG Leu 125	CTT	P GCG Ala
GTC Val 190	GCG Ala	GGC Gly	GTT Val	TCG Ser	GTC Val 110	CTC
ACC Thr	CAG Gln 175	CCG Pro	CAG Gln	AAG Lys	61y	GAT : ASP : 95
ACC Thr	GTA Val	AAG I.ys 160	GTG Val	CGC Arg	ACC Thr	TTC Phe
GTC . Val	AAA Lys	ACG Thr	GAA Glu 145	CCG Pro	TAT Tyr	GGC Gly
ATC Ile	TCC Ser	GCC Ala	GCA Ala	ATG Met 130	GAC Asp	AAT Asn
GAG Glu 195	GCC Ala	AAT Asn	GCC Ala	GGC Gly	ATG Met 115	GCC Ala
CCG (GTG Val 180	CCG Pro	GAT Asp	CGC Arg	AAG Lys	GGA Gly 100
GTC . Val	CTG Leu	ATC Ile 165	GGC Gly	GTG Val	ACC	ACC Thr
ATG Met	CTC Leu	ACC Thr	GAC Asp 150	CTG Leu	TCC Ser	GGC Gly
ACC Thr	GCC Ala	TAT Tyr	CGC Arg	AAC Asn 135	TTT Phe	GCG Ala
CGC Arg 200	GGT Gly	CGC Arg	ATG Met	CCG Pro	ATC Ile 120	CGC Arg
GAC Asp	CTC Leu 185	GTG Val	CCG Pro	TTG Leu	GGC Gly	CTC Leu 105
688	640	592	544	496	448	400

GGC Gly	CAG Gln	CGC Arg	TTC Phe 250	C'I'T' L'eu	ACC Thr	CAC His
GAA Glu	GAA Glu	AAC Asn	CCG Pro	l' GTC 1 Val 235	C GAC r Asp	s Thr
GAC Asp 300	ATG Met	GTG Val	CTC) G1y	C AAG p Lys 220	C GAA r Glu
GTC Val	GGC G1y 285	CTG	GTT Val	C CAG	G GAT S ASP	A AAG u Lys 205
GCC Ala	GCC 'Ala	ATG Met 270	GCC Ala	ACC Thr	r GGC 5 Gly	G ATG s Met 5
GAT Asp	GAT Asp	AAC Asn	GCC Ala 255	: ATC	G'FG Val	: Leu
CTG Leu	ATC Ile	CCG Pro	CTT Leu	GAC Asp 240) CGC Arg	G CAG
CGC Arg 305	GAA Glu	ACC Thr	CTG Leu	GTG Val	CAT His 225	GGC GIY
GTC Val	GTG Val 290	CGT Arg	GTG Val	CCG Pro	ATC Ile	Phe 210
AGG Arg	CTC Leu	ACC Thr 275	GAA Glu	GGC Gly	CGC Arg	GGC Gly
GCT Ala	AAT Asn	GGC Gly	GGT Gly 260	GAT Asp	ATC Ile	GCC Ala
TCG Ser	GCC Ala	CTC Leu	TCC	CCG Pro 245	ACC Thr	GAC Asp
AAG Lys 310	CGT Arg	ATC Ile	GAC Asp	TCA Ser	GGC Gly 230	CTC Leu
CTC Leu	CTT Leu 295	CTC	GTC Val	TCG Ser	CAG Gln	ACG Thr 215
AAG Lys	GCA Ala	ACC Thr 280	ACC	ACC Thr	GGC Gly	GTC Val
GGC Gly	GGC Gly	TTG Leu	ATC Ile 265	GCC Ala	AAG Lys	GAG Glu
1024	976	928	880	832	784	736

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ATG G Met G 410	ACG (Thr V	TCG Ser 1	GCA Ala	G]y	GTC Val 330	GPC Val
1 419 0 000 0	GTT (Val <i>l</i> 395	C'FG Leu	CGC Arg	CTC Len		Val 315
GGC CTT GC c Gly Len Ala	GCA . Ala '	ACG Thr 380	GGC Gly	GAC Asp	GCG Ala	: Gree Val
	ACC Thr	GTT Val	(:'I'T Leu 365	GAA Glu	ATT Ile	
GCG (Ala (CAT' His	CGC Arg	GAA Glu	CTG Len 350	r GCC Ala	3 CCG 5 Pro
GAA Glu 415	CTC Leu	GGC G1y	GCC Ala	a CGC Arg	2 GCC a Ala 335	0 G1
AAG I.ys	GAT Asp 400	CGC Arg	AAC Asn	GTC Val	C TCC a Ser	CCG CCG GAA CGT Pro Pro Glu Arg 320
CCG Pro	CAT His	CCC Pro 385	GGC Gly	C AAG L Lys	C TTC r Phe	T GCG g Ala 0
GTG Val	CGT Arg	GAC Asp	GTC Val 370	G GAA S Glu	C GCG e Ala	G CCG a Pro
ACG Thr	ATC Ile	GGC Gly	GAT Asp	A TCG 1 Ser 355	G GAA a Glu	G TCG o Ser
GTT Val 420	GCG Ala	AAG Lys	TGC	GAT Asp	A GGC u Gly 340	G ATG
GAC Asp	ATG Met 405	GGA Gly	ACC	l CGT D Arg	C GAA Y Glu 0	'G A''C t Tle 325
GAC Asp	AGC Ser	CTG Leu 390	GAA Glu	r CTG g Leu	A ACC u Thr	'C GAC e Asp 5
AGT Ser	TTC Phe	GG G1 ₁	4 GGC 1 G1y 375	GC Al	C GTG r Val	0.0
AAC Asn	CTC Leu	c GGC Y Gly	C GAG / Glu	A GCG a Ala 360	G ATG	BAA TAT Slu Tyr
ATG Met 425	GTG Val	C GGC	G ATG u Met	G GTC a Val		
e,	<u> </u>	× 0	ក់ជ	rc 11	GAC Asp 345	CCG Pro
1360	1312	1264	1216	1168	1120	1072

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Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly 430 GCA AAG ATC GAG TTG GCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC 1408 GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA TATTATTATTTGC Ala Lys Ile Glu Leu Ser Ile Leu 445 GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT CTTCCATACG 1522 GAGATTGGGC AGGAAATGATC AAAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC 1582	Ile A GCA A Ala L GAGAT	AG AU YS Il YS Il	r Ser Phe Pro Glu Pl 430 C GAG TTG AGC ATA CT e Glu Leu Ser Ile Le 445 ATTATTACCG GTTGGTCT	TC ATG GAC ATG A'TG CCG GGA TTG GGC THE MET ASP MET MET Pro Gly Leu Gly 435 TC TAGTCACTCG ACAGCGAAAA TATTATTTGC TC TAGGGGGGTTT AATGTCCAAT CTTCCATACG TTT TAGAAGGAA'T TGCTAGAGCA GCGACGCCGC	1408 1462 1522 1582
	E'l'GEC'	L.1.7.7.1.d	AUGACUTICAU TECTGAGAAA TEGGCCTCGC A	IGC A	1673

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TYPG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG	AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu 80	GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT	CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC	ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT	AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC	GTGATCGCGC CAAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG
Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala		Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg	Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp	The Pro Gly Asp Lys Ser The Ser His Arg Ser Phe Met Phe Gly Gly	Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg	Met Ser His Ser Ala Ser Pro
95		60 65	40 55	25	10	1
342	294	246	198	150	102	54

CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GArg Asp His Thr.•Glu Lys Met Leu Gln Gly Phe Gly A 200	GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG (Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu F 185	GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala 170	Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn 155	Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala 140	GGC GAC GCC Gly Asp Ala	Arg Len Thr Met Gly Len Val Gly Thr Tyr Asp Met 105
GGC Gly	GAG Glu 195	GCC Ala				
GCC GAC Ala Asp	CCG GTC Pro Val	GTG CTG Val Leu 180	CCG ATC Pro Ile 165	GAT GGC Asp Gly	CGC GTG	AAG ACC
CTC ACG Leu Thr 215	ATG ACC Met Thr	CTC GCC Leu Ala	ACC TAT Thr Tyr	GAC CGC Asp Arg 150	CTG AAC Leu Asn 135	TCC TTT Ser Phe
678	630	582	534	486	438	390

AAG Lys	GCA Ala	ACC Thr 280	ACC Thr	áCC Thr	GGC GTy	GTC Val
GGC Gly	GGC G1y	T''I'G	: ATC ::I1e 265	: GCC : Ala	C AAG Y Lys	C GAG l Glu
GTC Val	GGC Gly	CAG Gln	e Arg	C TTC a Phe 250	G CTT s Leu	u Thr
GTC Val 315		GAA Glu) AAC J Asn	C CCG e Pro O	T GTC u Val 235	C GAC
GTT Val	GAA GAC Glu*Asp 300	ATG Met	C GTG n Val	G CTC o Leu	1 G1y 5	
CCG Pro	val	3 GGC 5 Gly 285	G CTG 1 Leu	u Val	je eAG y Gln	
CCG Pro	Ala	C GCC 7 Ala 5	G ATG n Met 270	T GCC		GAT G Asp G
GAA Glu	C GAT a Asp	C GAT a Asp	G AAC t Asn 0		ACC A Thr I	GGC G Gly V
A CGT 1 Arg 320	T CTG p Leu			GCC (Ala I 255	ATC (Ile /	GTG (Val
		ATC (Ile (CCG .	CTT Leu	GAC Asp 240	CGC Arg
GCG (Ala F	CGC Arg 1	GAA Glu	ACC Thr	CTG Leu	GTG Val	CAT His 225
CCG Pro	GTC Val	GTG Val 290	CGT Arg	GTG Val	CCG	ATC Ile
TCG Ser	AGG Arg	CTC Leu	ACC Thr 275	GAA Glu	GGC Gly	CGC
ATG	GCT Ala	AAT Asn	GGC Gly	GGT Gly 260	Asp	ATC
ATC Ile 325	TCG Ser	GCC Ala	CTC Leu	TC Sej	CC Pr 24	AC Th
GAC Asp	AAG Lys 310	CGT Arg	ATC Ile	C GAC	G TCA o Ser 5	C GGC r Gly 230
GAA Glu	CTC L'eu	CTT Leu 295	CTC Leu	GTC Val	A TCG	C CAG 7 Gln
		O. 2	<u> </u>	ьO	۳ G	n G
1014	96	9	&	m	-1	- 1
	66	918	870	822	774	726
	•					

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	AAC ATG Asn Met 425	CTC GTG Leu Val	GGC GGC	GAG A Glu M	GCG C Ala V 360	ATG (Met /	TAT (
	G ATC t Ile			ATG 7	CTC (Val ,	GAC Asp 345	CCG Pro
		ATG (Met (410	ACG Thr	TCG Ser	GCA Ala	GGG Gly	GTC Val 330
٠.	GCC , Ala ,	GGC Gly	GTT Val 395	CTG Leu	CGC Arg	CTC Leu) CTG Leu
	ACG Thr	CTT Leu	GCA Ala	ACG Thr 380	GGC Gly	GAC Asp	3 GCG 1 Ala
	TCC	GCG Ala	ACC Thr	CTT Val	CTT Leu 365	C GAA 9 Glu	G ETT a Ile
	TTC Phe 430	GCG Ala	CAT	CGC Arg	r Gaa u Glu 5	A CTG u Leu 350	'T' GCC e Ala
	CCC Pro	GAA Glu 415	CTC	c GGC g Gly	A GCC u Ala	G CGC u Arg	
	GAA Glu	AAG Lys	C GAT 1 Asp 400	C CGC Y Arg			GCC T Ala S 335
	TTC Phe					GTC , Val	TCC Ser
		CCG (CAT His	CCC Pro 385	GGC Gly	AAG Lys	TTC Phe
	ATG (Met i	GTG Val	CGT Arg	GAC Asp	GTC Val 370	GAA Glu	GCG Ala
	GAC Asp 435	ACG Thr	ATC Ile	GGC Gly	GAT Asp	TCG Ser 355	GAA Glu
	ATG Met	GTT Val 420	GCG Ala	AAG Lys	TGC	GAT Asp	1 GGC 1 Gly 340
	ATG Met	GAC Asp	ATG Met 405	GGA Gly	AC Th	CG Ar	C GAA Y Glu
	CCG Pro	GAC Asp	AGC Ser	CTG Leu 390	C GAA r Glu	T CTG	A ACC u Thr
	GGA Gly	AGT	TTC Phe				
	∀ ⊅	ř	e C	GGC Gly	GGC Gly 375	GCA Ala	GTG Val
	1350	1302	1254	1206	1158	1110	1062

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440 THG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu 445

1400

TAITTAITTAC GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT 1460

CHITCCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT

1500

Figure ഗ

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51 45 99	1MESITIQPIARVDGTINLPGSKTVSNRALLLAALAHGKTVLTNL 44 51 LEGEDVINTGKANQAMGARIRKEGDTWIIDGVGNGGLLAPEAPLDFGN 98 1::: : : : : : : : : 45 LDSDDVRHMI.NALTALGVSYTLSADRTRCEIIGNGGPLHAEGALELFLGN 94 99 AATGCRLTMGI.VGVYDFDSTFIGDASLTKRPMGRVI.NPLREMGVQVK.SE 147 1:1: : ::: : :::::	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
45		# ~ (
وو	AATGCRLTMGLVGVYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVK.SE 1	17
95	AGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDALRLGGAKITYLE 144	14
148	148 DGDKLPVTLKGPKTPTPITYRVPMASAQVKSAVLLAGLNTPGITTVIEPI 197	7
145	145 QENYPPLRLQGGFTGGNVDVDGSVSSQFLTALLMTAPLAPEDTVIRIKGD 194	4
158	198 MTRDHTEKMLOGFGANLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSS 247	7
195	195 LVSKPY1DITELNEMKTEGVEIENQHYQQEVVKGGQSYQSPGTYLVEGDAS 244	4

446 KIE	377 }	396 1	J J J	346	288	296	اد <u>څ</u> ن	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
446 KIELSDTKAA* 456	377 AEIATYNDHRMAMCFSLVAL.SDTPVTILDPKCTAKTFPDYFEQLARISQ 425	396 AAVATHLDHRIAMSFLVMGLVSENPVTVDDATMIATSFPEFMDLMAGLGA 445	NIYNWRVKETURLEAMATELRKVGAEVERGHDVILI DITTURE	GLEELRVKESDKLSAVANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASG 395	288 CWGDDYISCTKĞELNAIDMDMNHIPDAAMTIATAALFAKGTTRLR 332	AGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAEGATVMN 345	•	240 TAFPLVAALLVEGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRL 295
	25	76 45		ر م	32	345	287	295

300	_	151
300	PLVAALLVPGSDVTILNVLMNPTRTGLILTLQEMGADIEVINPRLAGGED	251
250	-	201
250	DHTEKMLQGFGAHLTVETDADGVRTIRLEGRGKLTGQVIDVPGDPSSTAF	201
200	RMPLTLIGPKTANPITYRVPMASAQVKSAVLLAGI,NTPGVTTVIEPVMTR	151
200	RLPVTLRGPKTPTPITYRVPMASAQVKSAVLLAGLNTPGITTVIEPIMTR	151
150	TGARLTMGLVGTYDMKTSFIGDASLSKRPMGRVLNPLREMGVQVEAADGD	101
150	TGCRLTMGLVGVYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVKSEDGD	101
100	LEGEDVINTGRAMQAMGAKIRKEGDVWIINGVGNGCLLQPEAALDFGNAG	51
100	LEGEDVINTGKAMQAMGARIRKEGDTWIIDGVGNGGLLAPEAPLDFGNAA	51
50		
50		

α	15	86	13	51	<u> </u>	301	105	
18 II 449	51 DTKAA* 456	98 HLDHRIAMSFXVMGLAAEKPVTVDDSNMIATSFPEFMDMMPGLGAKIELS 447	OI HEDHKIAMSELVMGLVSENPVTVDDATMIATSFEEFMDLMAGLGAKIELS 450	51 RVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLGGGTVAT 397	SEL KVKESDRLSAVANGLKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAVAT 400	301 VADLRVRASKIKGVVVPPERAPSMIDEYPVLAIAASFAEGETVMDGLDEL 350	01 VADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAAFAEGATVMNGLEEL 350	
		47	50	97	00	50	50	

840	CTCATCTTGA		TGAACCCAAC CCGTACTGGT		GTTCCGACGT CACCATCCTT AACGTTTTGA	GTTCCGACGT
780	CTTGTTCCAG		ATGITTCCAGG TGATCCATCC TCTACTGCTT TCCCATTGGT TGCTGCCTTG	TCTACTGCTT	TGATCCATCC	ATGTTCCAGG
720	CAAGTGATTG		GTCGTGGTAA	CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA	GCGTACCATC	CTGACGGTGT
660	GAGACTIGATIG	CCTTACCGTT		GTGACCACAC TGAAAAGATG CTTCAAGGTT TTGGTGCTAA	TGAAAAGATG	GPGACCACAC
600	ATCATGACTC	'I'ATCGAGCCA	TCACCACTGT TATCGAGCCA	ACCCCAGGTA	THETGETTIGE TIGGTETEAAC	TECTGCTTGC
540	AAGTCCGCTG	CGCTCAAGTG	CTATGGCTTC	TACAGGGTAC	GCCAATCACC	AGACTCCAAC
480	CGTGGACCAA	AGTTACCTTG	GAAGACGGTG ATCGTCTTCC	GAAGACGGTG	TGGGTGTGCA GGTGAAGTCT	TGGGTGTGCA
420	CTTCGCGAAA	GTTGAACCCA	TGGGTCGTGT	THUGTGAUGU TTCTCTCAUT AAGCGTCCAA	TTCTCTCACT	TTGGTGACGC
360	AGCACTTTCA	CGATTTCGAT	TTGGTGTTTA	CCGTTTGACT ATGGGTCTTG	CCGTTTGACT	CAACTGGTTG
300	GGTAACGCTG	TCTCGATTTC	CTGAGGCTCC TCTCGATTTC	CTCCTTGCTC	TAACGGTGGA	APGGPGTFGG
240	TGGATCATTG	AGGTGATACT	GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAGGA	GGTGCCAGAA	C GCAAGCTATE	GTAAGGCTAT
180	ATCAACACTG	TGAAGATGTT	TTTTGGAAGG	TGAAACTCGT ATCACCGGTC	; T'GAAACT'CG'I	TUGUTAGUGG
120	TTTGGAGGTC	GTCCTTCATG	TCTCCCACAG	TATTCCAGGT GACAAGTCTA		GAACCGTCCG
60	GGTCTTTCTG	TAAGTCCTCT	CHAISSCIAN CSSISCAASC ASCUSTUCAG CAACTGCTCG TAAGTCCTCT	AGCCGTCCAG	a caalacaabt	CCATOGCTC

1377	TGAGCTC		CCGACACTAA	A'FCGAACTCT	TIGGCTIGGTICT TIGGAGCTIAAG AITCGAACTCT CCGACACTAA GGCTGCTTGA	TGGCTGGTCT
1320	ATGGATTTGA		CTACTAGCTT	ACTATGATCG	CHGHTPACTGT TGATGATGCT ACTATGATCG CTACTAGCTT CCCAGAGTTC	CTGTTACTGT
1260	TCTGAAAACC	GGGTCTCGTT	TCCTCGTTAT	GCTATGAGCT	CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT	CCCACCTCGA
1200	GCTGTCGCTA	TTCTGGAGCA	TCGGTAACGC	GGTAAGGGTC	TOGTGOGTGG TOGTCCTGEC GGTAAGGGTC TCGGTAACGC TTCTGGAGCA	TCGTGCGTGG
1140	ACTTCTCTCG	TGAAGGTGAG	TTGATTGCGA	CTCAACGGTG	CTGTCGCAAA CGGTCTCAAG CTCAACGGTG TTGATTGCGA TGAAGGTGAG	CTGTCGCAAA
1080	CGTCTTTCTG	GGAAAGCGAC	TCCGTGTTAA	TTGGAAGAAC	GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTTAA GGAAAGCGAC	GTGCTACCGT
1020	TTCGCTGAAG	TGCAGCTGCA	TTCTCGCTGT	GAGTATICCAA	GPGCPCCPPC TATGATCGAC GAGTATCCAA TTCTCGCTGP PGCAGCTGCA	GTGCTCCTTC
96(CCAGAAGACC	"GTTACTGTT	CTTTGAAGGG	CGTTCTTCTA	ACGTGGCTGA CTTGCGTGTT CGTTCTTA CTTTGAAGGG TGTTACTGTT	ACGTGGCTG/
90	GGTGGAGAAG	ACGTCTTGCT	TGATCAACCC	GACATCGAAG	CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT	CTCTGCAGG/

60

Figure 9

Ala Tyr Pro GCT TAT CCG CGCGly CGATTGCTTTC AATTGAAGTTT TCTCCG ATG GCG CAA GTT AGC AGA ATC AGATCTATCG ATAAGCTTGA TGTAATTGGA GGAAGATCAA AATTTTCAAT CCCCATTCTT Lys AAAVa] GTG CAG Ser TCT Gln Ile ATT TOG TOG TCG TGG GGA TTG AAG Pro CCC AAC Asn Ser Ser Ser Trp Gly Leu Lys Lys Leu TTAPro CCA THE GTT Ser Val TOT CTT ATC TCC AAT Ser Leu Ser TCT Ile Met Leu CTG Ser Ala Gln Val Ser Arg Ile Cys Lys AAG Asn Leu Thr Gln Gln CTC ACG 20 AAG CAG Ser Lys TCG AAA Ser AGT CAG Gly GGG CAT TCC Ser Ser Met ATG CCA Pro AGT TGC Thr ACG Arg CGA Gln CAA Asn AAT 257 209 161 113 60

Figure 10

TCC Ser 90	ACG Thr	TrpA Leu
GGT Gly	GCG Ala 75	ATT Ile
CTT Leu	GAG Glu	60 60
ATT Ile	AAA Lys	
AAG Lys	GCG Ala	TCT GAG Ser Glu
7"1"G L'eu 95	TCG Ser	L'eu
CCT Pro	GAG Glu 80	CGT
GGC Gly	ATT GTA (Ile Val I	CCT Pro 65
TCC Ser	GTA Val	CTT Leu
AAG Lys	CTT Leu	AAG Lys
TCT Ser 100	CAA Gln	GTC Val
r C'ra 1	CCC Pro 85	ATG Met
TCA Ser	ATT Ile	TCT Ser 70
TCA AAT Ser Asn	ATT AGA Ile Arg	TCT Ser
AGA Arg	GAA Glu	GTT Val
ATT Ile 105	ATC Ile	TCC Ser
401	353	305

 \bigcirc

402

Figure

	TICT ATC TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG T Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys F 45	TICA AGT TITE CTT GTT TETT GGA TCT AAA AAA CTG AAA AAT TCA C Ser Ser Phe Leu Val Ehe Gly Ser Lys Lys Leu Lys Asn Ser <i>t</i> 30	ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT I Thr Len Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro I 15 20	Met Ala Gln Ile Asn Asn Met Ala Gln Gly I 1
ACA CCC TCC TTCC	TTT ATG CAA Phe Met Gln 55	CTG AAA AAT Leu Lys Asn 40	CAA GTT Gln Val 25	ATG GCT CAA GGG Met Ala Gln Gly 10
233	193	145	97	49

AGA Arg 100	GAG Glu	GTG Val	Asp
A'l"I' I l e	ATT I l e 85	i GCT /	Ser
C	TCA Ser	ACA Thr 70	Ile
	GGC Gly	GCA Ala	Phe 55
	TCA GGC ACT GTT Ser Gly Thr Val	CAG Gln	Met
	GT" Va]	GCA CAG ££G CCT TCT Ala Gln Lys Pro Ser 75	Asp Ser Ile Phe Met Gln Lys Phe Cys 55
	Lys.Leu 1	CCT	AAG Lys
	TTG	TCT Ser 75	T'T'T Phe
	Pro Gly Ser	GAG Glu	TGT Cys 60
	GGC Gly	GAG ATA GTG Glu Ile Val	TCC
	TCT Ser	GTG Val	TTT Phe
	AAA Lys 95	'I''FG Leu	AGG Arg
	TCA Ser	CAA Gln 80	ATT Ile
	TTA	CCC Pro	AGG ATT TCA Arg Ile Ser 65
	TCT	ATT Ile	GCA Ala
	AAT Asn	AAA Lys	TCA Ser
<u>ω</u>	ω	2	2
352	345	297	249

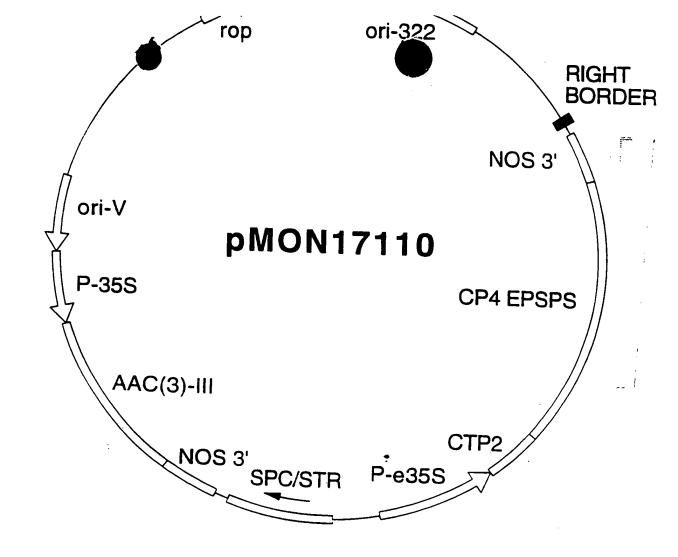


Figure 13

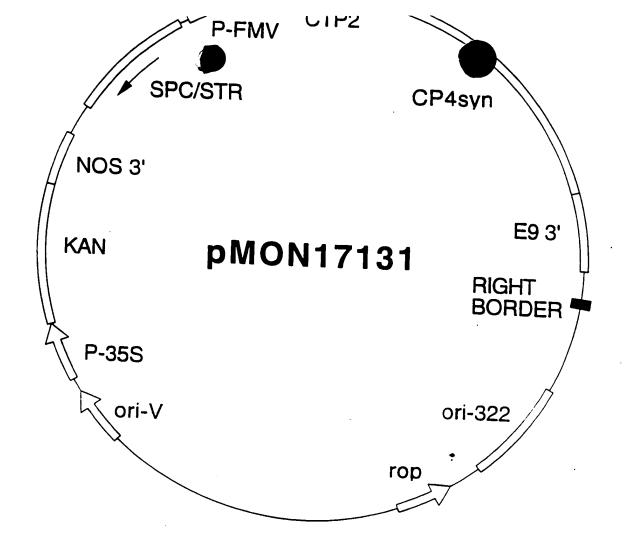


Figure 14

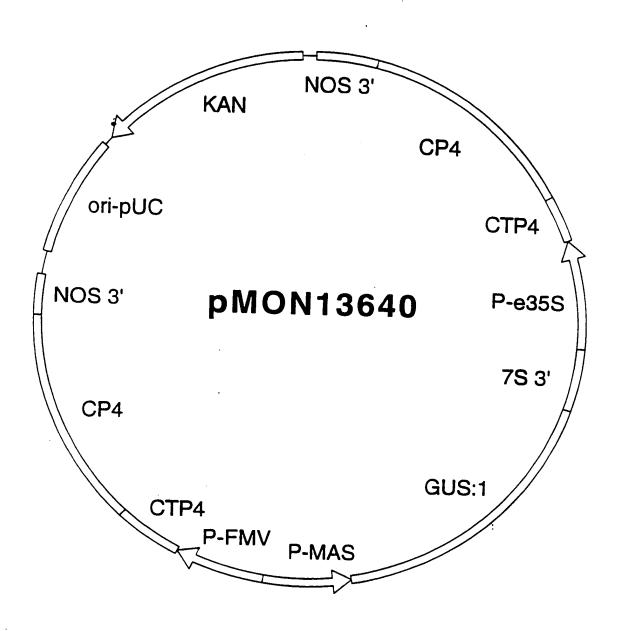


Figure 15

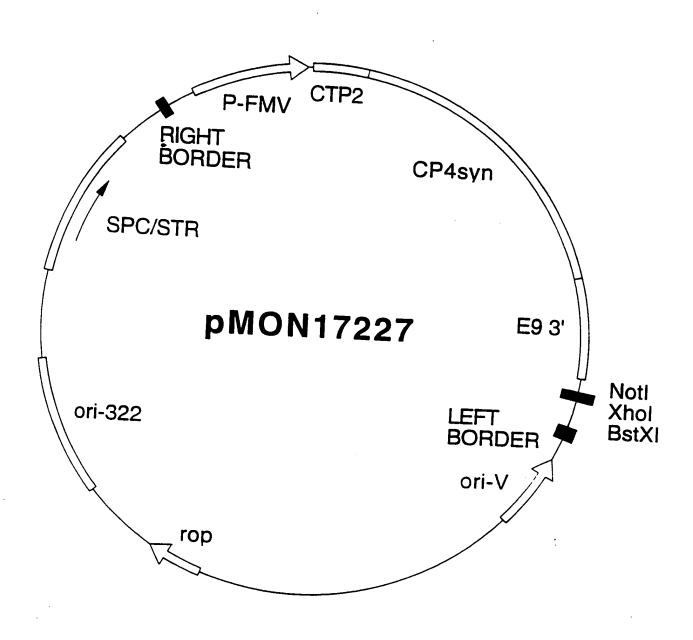


Figure 16

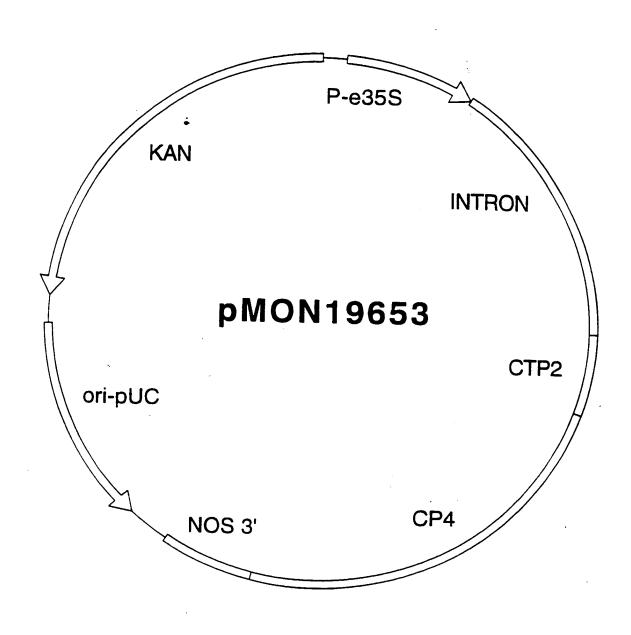


Figure 17

48

96

18 Figure

of

384	432	480	528	576	624	672
GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG ASP Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu 120	AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGC GGA GAG TTT ACA Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr 130	CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asb Tyr Val Ser 145 155 150	CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA GIN Ile Lys Ser Ala Val Leu Leu Ala Gly 177	GCT GAG GGC ACA ACA ACT GTA ACA GAG CCC CAT AAA TCT Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser 180	TCT GCT TTT GGC GTT AAG CTT Ser Ala Phe Gly Val Lys Leu 200	CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp 210

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720	768	816	864	912	096	1008
CTT GCT GCT Leu Ala Ala 240	GTA GGT TTA Val Gly Leu 255	G GGG GCA st Gly Ala	T TAT GGA o Tyr Gly	C GGA GGA e Gly Gly	3 CTT CTT Leu Leu 320	GAG CTA Glu Leu 335
TTT TTC C	AAA AAC G1 Lys Asn Ve	CAA AAC ATG Gln Asn Met	GCA GAG CCT Ala Glu Pro 285	GTT GAA ATC Val Glu Ile 300	ATC ATC GCG Ile Ile Ala	GAC GCG GCA Asp Ala Ala
GCC GCG Ala Ala 235	GTA TTG Val Leu 250	GTC CTT Val Leu	AGC GGT Ser Gly	AAG GCA Lys Ala	ATC CCT A' Ile Pro I	ATT AAG GA Ile Lys As 330
. [• 0]	C AGA ATT r Arg Ile	T ATT GAT e Ile Asp 265	r GCT GAT r Ala Asp 280	A TCT CTA Ser Leu	GAT GAG Asp Glu	ACC GTT Thr Val
SGA GAC ATT SIY ASP Ile 230	CCA AAC AGC Pro Asn Ser 245	ACA GGT ATT Thr Gly Ile	AA CCA TCT ys Pro Ser	GAA ACG TCA Glu Thr Ser 295	CGT TTA ATT Arg Leu Ile 310	AA GGA ACC u Gly Thr
F GTT CCT GGA	ATG GTT Met Val	ACT CGG Thr Arg 260	GAA ATC AAA Glu Ile Lys 275	ATT ATA	ATT CCG	ACT CAG GCG GAA Thr Gln Ala Glu 325
ATM TWM GTM Ile Phe Val 225	GGC GCG Gly Ala	AAT CCG Asn Pro	AAA CTT GAA Lys Leu Glu 275	GAT TTG A ASP Leu 1 290	GAT ATC ASP IIe 305	GCG ACT Ala Thr

Figure

SHEET 3 of

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1056	1104	1152	1200	1248	1287
CTT CGC Leu Arg	T TAT 1 Tyr	A GAT Y Asp	3 GAG 1 Glu 400	A ACC Thr	v.
GAG Glu 350	AAG GTT Lys Val	AGC CAC GGA Ser His Gly	ACG GAG Thr Glu	TAT CCA Tyr Pro 415	
r TCT Ser	ATG Met 365		ATA ACG	TCT Ser	TGA
1 va]	T GGA P Gly	G TCC 1 Ser 380	Cys	GTT	TCC
CT-GT hr Va	GCA GAT Ala Asp	GCA GTG Ala Val	T TCC a Ser 395	T CAC e His O	A AAA S Lys
3AT'A	ACA G(Thr A]	GCT GC Ala Al	ATT GCT Ile Ala	GCC ATT (Ala Ile 1 410	TCG AAA Ser Lys 425
AAA GAA ACA AAC CGITATIT GATACT GITT GITT IVS Glu Thr Asn Arg Ile Asp Thr Val Val 340	CCG Pro 360	66C G1 y	GGT A	GAT G Asp A	CTT To Leu Se
CCGT	GAA Glu	GGC G1y 375	CTT	ACG Thr	AAG Lys
A EAC	A A'FT 1 Ile	AAA I I,ys	ATG Met 390		AAT Asn
A ACA	r GAA a Glu	AAA CAA ACG TTG Lys Gln Thr Leu 370	CGA ATC GGA ATG Arg Ile Gly Met	ATT GAA ATC GAG Ile Glu Ile Glu 405	CAT TTA His Leu 420
GAA GG11 34(GGT GCT Gly Ala 355	ACC Thr	GGA G1y	ATC Ile	CAT His 420
AAA Lys	GG1 G1y 355	CA4 Gln	ATC Ile	GAA Glu	GAG Glu
AAA GTG A	AAG CTG (Lys Leu (AAA Lys 370	CGA Arg	АТ"Г I 1 е	TTC (
AAA Lys	AAG Lys	GGC G1 <i>y</i>	CAT His A	CCG	Tric

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	Thr Arg	Val	A'IC I'le 65	GAA Glu	A]a	д нр	D 3 7
	Arg	AAC Asn	AAA Lys	- w	•	-	ATG Met
	TT'A Leu	ACG	_	o C C	Ser Leu 35	GAA Glu	_
	TTA TTG Leu Leu 100	G CCA r Pro	AA GAT U Asp	TGT (Leu 35	Val	_
	G GCA u Ala o	•	AT (CGT CGT Arg Arg	GCT Ala	CCG Pro 20	GAA Glu
•		CAT (His (GAA GAT GAT (JAA Glu Asp Asp Glu 70	CGT Arg			CAA Gln 5
	GGT 1	CAA Gln	GAA Glu 70	ACG Thr	GAA GGT Glu Gly	Asp	A ATC
	TTG Leu .	GTA Val	AAA Lys	ATG Met 55	GTA Val	T AAG O Lys	'C ATT e Ile
	TTA Leu	TTG Leu	TT! Let	GAC Asp	A TCT l Ser 40	G TCA	PT G le A
	AGT Ser 105	TAT Tyr	TTA GTT GTG Leu Val Val	C ATT D Ile	T ACT r Thr 0		GAT A
	GGT Gly	ACA Thr 90	r GT Va	T TI		ATG A Met T 25	ATT
	TTA Leu	A GGT Gly	H A	TTC CGA Phe Arg	ATA TAT AAG Ile Tyr Lys	ACA (Thr I	TCA Ser 10
	a GGT 1 Gly	T AAT Y Asn		CGA (Arg H	TAT Tyr	CAC His	GGT Gly
		AT T	TCC (Ser H	CAC His		CGT Arg	GGT CCG Gly Pro
		TCT (Ser (CCA Pro	TTA Leu	CCA Pro 45	GCA Ala	TTA Leu
	GAA i Glu s 110	GGT Gly	GGA Gly	GGT Gly	CTA Leu	ATC Ile 30	AAG Lys
	AGT Ser	ACG Thr 95	TAT Tyr	GTA Val	CTT	ATG Met	3 GGC 8 Gly 15
	GTT Val	ACA Thr	CAA Gln 80	GAA Glu	r GGC ı Gly	G TTG	iC GAA Y Glu 5
				L 18	Υ Ω	น ดี	AA lu
	336	2	N	L .			
	6	288	240	192	144	96	48

SHEET 1 of 4

GCA Ala	CGA Arg	AGT Ser	CAA Gln	ТАТ Туг 145	AGA Arg	Ten Len
GAA Glu 210	AAT Asn	TTG Leu	ATG Met	Thr	CCA Pro 130	1 Ser
GGG Gly	CAT His 195	TTT Phe	GAA Glu		A TTG	P GGC C Gly 115
T'TA L'eu	ACT Thr	TCT Ser 180	GTT Val	CCA: יויים Pro Leu	3 AAA 1 Lys	C GAT Asp
TCA Ser	GAG G] u	AAG Lys	GCA Ala 165	A'I''I'		
ATT I]e	ACG Thr	GAA Glu	AGT Ser	' A'I'T ! Tle !150	CTT ATG Leu Met	GTTP THEA Val Ser
AAT Asn 215	ATG Met	CCG Pro	GCA Ala	AAG Lys	GAT Asp 135	A ATT
ACA Thr	TTC Phe 200	ACC Thr	CAA Gln	CCA	r GCG Ala	r GGT e Gly 120
ACC Thr	AAA Lys	ATC Ile 185	GTA Val	TCT	AAT Asn	f AAA ' Lys
CCT	CAT His	ATT Ile	AAA Lys 170	GTC Val	ATT	AGG Arg
GAA Glu	TTT Phe	AAA Lys	AG'l' Ser	ATA Ile 155	GAA Glu	CCA
GCA Ala 220	AAT Asn	GAA Glu	GCC Ala	AAA I.ys	GGT Gly 140	ATG Met
ATT Ile	ATT Ile 205	TTA Leu	ATT Ile	GGT Gly	ATT Ile	Asp 125
CGA Arg	CCA Pro	GAT Asp 190	TTA Leu	ATA Ile	GAA Glu	CGT
TAC Tyr	ATT Ile	GTA Val	TTT Phe 175	AAT Asn	GAT Asp	GTC Val
ATT Ile	GAA Glu	AGT Ser	GCA Ala	TAT Tyr 160	AAT Asn	TTG
672	624	576	528	480	432	384

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ATA Ile	ACA Thr 305	CCT Pro	AAA Lys	ASN	'I'I'I' Phe	AAA Lys 225
GCA Ala	ATC Ile	ACT Thr 290	ATG Met	· GTT	l'ATT E Ile	A CC
TTA CTT	GAA Glu	GCT Ala	GGC G1y 275	Gly	r GTT e Val	r gcz 5 Ala
	GGA GAA Gly Glu	TCT Ser	GG1 G1y	ATC T1e 260	r GCA Ala	A GAT a Asp
TGT Cys 325		AT"l' Ile	GGT AAT Gly Asn	AA'I' Asn	A GCA A Ala 245	Pho
ACA Thr	Tr'FA Leu 310	CGT Arg	ATC Ile	Gln		P CAT B His 230
CAA Gln	GTT Val	ATT Ile 295	CAA Gln	ACA Thr	CTT ATC Leu Ile	AAA CCT GCA GAT TYP CAT GTT Lys Pro Ala Asp Phe His Val 225
GCA Ala	CCA Pro	CAA Gln	CTT Leu 280		ACA Thr	r CCT
GTT Val	AAA GCA Lys Ala	TAC Tyr	TTC Phe	CGT TCA Arg Ser 265	CCA Pro	
GGC Gly 330		ACA Thr	AAT Asn	GGT Gly	GGA Gly 250	GGC GAT Gly Asp
ACG Thr	ATT Ile 315	CCA Pro	CAA Gln	ATT Ile	AGT Ser	APT 11e 235
AGT Ser	GAT Asp	ATG Met 300	ACA Thr	ATT Ile	GAT Asp	TCA Ser
ACA Thr	GAA Glu	CTT Leu	ACT Thr 285	GAT Asp	GTA Val	TCT
ATT Ile	CTG Leu	CAA Gln	GGT Gly	ATT 11e 270	ACA Thr	GCA Ala
AAA Lys 335	CCT	CCA Pro	GCT Ala	GTT Val	ATT Ile 255	GCG Ala
GAT Asp	GTA Val 320	ATA Ile	GAA [*] Glu	GAA Glu	CAT His	TTC Phe 240
1008	960	912	864	816	768	720

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CCA Pro	&GC Ser	ACT Thr 385	TTG Len	GAT Asp	GCC Ala
GGA Gly	GAG Glu	GAT ASD	AT". I 1 6 37(ATo Mei	: GAG a Glu
TTT Phe	CCT Pro	CAT His	A'I"P Ile	TTA Leu 355	GAG GAA Glu Glu
TTA Leu 420	CCF GTC Pro Val	CGA Arg	P ATT CAT CCG	AAC Asn	
CCA Pro	AAA Lys 405	ATA Ile	CCG Pro	TTG	AA.
T TTA CCA AAA CTA e Leu Pro Lys Leu 420	ETC AAA Ile Lys	CAT CGA ATA GGA ATG His Arg Ile Gly Met 390	Ser Glu 375	T'TA L'eu	val
CTA Leu	AAA Lys	ATG Met	GAA Glu 375	GGG Gly	Lys
AAG Lys	CAA Gln	ATG Met	TTT Phe	TTT Phe 360	TTA AAA GTA AAA GAA Leu Lys Val Lys Glu 340
CTT Leu 425	TTT Phe	CTT Leu	AAA Lys	GAA Glu	ACA Thr 345
TTA Leu	GAT Asp 410	GCA Ala	ACA Thr	TTA Leu	AAT Asn
CAA Gln	GCT Ala	GTT Val 395	ACA AAT Thr Asn	TTA CAA Leu Gln	AGA Arg
AAT Asn	TTT GAT GCT GTA AAT Phe Asp Ala Val Asn 410	GCT Ala	GCA Ala 380	CCA Pro	ATT Ile
GAG Glu	AAT Asn	TGT GTA Cys Val	ACA Thr	ACT Thr 365	GAT Asp
GGA Gly 430	GTA Val	GTA Val	GAT Asp	AAT Asn	ACA Thr 350
TAA	TCA Ser 415	CTT Leu	ATT Ile	GAT Asp	ACG Thr
	יוייויי Phe	TCA Ser 400	TTA Leu	GGA Gly	GCT Ala
1293	1248	1200	1152	1104	1056

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Consensus	B. pertussis	A. salmonicida	P. multocida	H. influenzae	r. entoercolitica	n. pheallomae	1100 . 1	11 CO 1		S Typhimurium	S. gallinarım				N tabacim	A. Thaliana	B name	A nidulane	S. CPI-VISIAE	בנ	┛.	Vao milita de população	I.BAA	C86C5d	
; ; ; ; ; ;		•				•		•				•	•						•	•				•	_
 	•	•	•	•	•		•	•	•	•	•									•	•				
1 1 1 1 1 1 1 1	•			•	•		•	•	•	•	•	•		•	•										
	MSGI,AVI.	ISIN	MIKDATAT	MEXT	MLESI	MESL	MESL	····MESL	MESL	MESL	AGAEEI	.KPSEI	.KPHEI	.KPNEI	.KASEI	.KASEI	VHP	LVYP	MVNEQ		MSHGASSRPA	MSHSASPKPA	MSHSASPKPA		
	DI. DA ARI ARG	SI EDICATION OF	TINDICVIEC	TLAPISAVEG	TI.HPTALTNG	TLOPIARVDG	TLQPIARVDG	TLQPIARVDG	TLQPIARVDG	TLQPIARVDG	VLQPIKEISG	VLQPIKEISG	VLXPIKDISG	VLQPIKDISG	VLQPIREISG	VLQPIREISG	GVAHSSNV	FKDIPADQQK		KRDKVQTLHG	TARKSSGLSG	TARRSEALTG	TARRSEALTG	50	

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Agrobacterium CP4 entoercolitica S. typhimurium salmonicida influenzae pneumoniae gallinarum A. nidulans esculentum B. subtilis multocida cerevisiae pertussis Consensus S. aureus S. typhi thaliana hybrida B. napus tabacum E. coli Z. mays PG2982 LBAA EVALPGSKSI ------PG-K--EVNLPGSKSV EVRLPGSKSL TINLPGSKSL TVNLPGSKSV TVNLPGSKSV TINLPGSKTV AINLPGSKSV AINLPGSKSV AINLPGSKSV TVKLPGSKSL TVKLPGSKSL TVKLPGSKSL TVKLPGSKSL LIKLPGSKSL LIKLPGSKSL TCAPPGSKS1 VVIPPGSKS EIEVPGDKSM ETHI PGDKS TVRIPGDKS1 EIRIPGDKSI EIRIPGDKSI SNRVLLLAAL SNRALLLAAL --R----L SNRALLLSAL SNRALLLAAL SNRALLLAAL SNRALLLAAL SNRALLLAAL SNRALLLAAL SNRALLLAAL SNRALLLAAL SNRILLLAAL SNRILLLAAL SNRILLLAAL SNRILLLAAL SNRILLLAAL SNRILLLAAL SNRALVLAAL SNRALILAAL THRAIMLASL SHRSVMFGAL SHRSFMFGGL SHRSFMFGGL SHRSFMFGGL AEGSTEITGL --G----ARGTTRLTNL AKGKTTLTNL AKGTTKVTNL AEGTTQLNNL ARGTTVLTNL AHGKTVLTNL ACGKTVLTNL SEGTTVVDNL GSGTCRIKNL PCGKTALTNL ACGKTVLTNL SEGTTVVDNL SEGRTVVDNL SKGRTVVDNL SEGTTVVDNL SEGTTVVDNL GEGQCKIKNL AEGVSTIYKP AAGTTTVKNF ASGETRITGL ASGETRITGL ASGETRITGL LDSDDTRVML L---D----LDSDDIRHML LDSDDVRHML LDSDDIRHML LDSDDIRHML LDSDDVRHML LDSDDVRHML LDSDDVRHML LDSDDVRHML LDSDDVRHML LNSEDVHYML LEGEDVINTG LSSDDIHYML LSSDDIHYML LNSDDINYML LLGEDCRRTM LPGADCLSTI LEGEDVINTG LSSDDIHYML LNSDDINYML LHSDDTEVML LHSDDTKHML LEGEDVINTG AALRQL.GVS AALTQL.GVK NALKEL.GVT NALKAL.GVR NALQAL.GVK NALSAL.GVH NALTAL.GVS NALSAL.GIN NALSAL.GIN NALSAL.GIN GALRTL.GLS GALKTL.GLH GALKTL.GLH GALKTL.GLH DALKRL.GLN DALKKL.GLN NALERLGAAT TAVHELKGAT DIFRHL.GVE DCFRKM.GVH RAMQAM.GAK KAMQAM.GAR RAMQAM.GAK

Figure 20

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COnseilsus	GGDY	Salilonicida GSGEX	ET LOS COLOR TENNESTER COLOR	multocida Teneralia		r. enfoercolitica GKNDI		h. pheumoniaeGSNDI	K. pneumoniaeGSNDI	E. coliGSNDI K. pneumoniaeGSNDI	S. typhiGQNEI S. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	S. typhimuriumGQNEI S. typhimuriumGQNEI S. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	S. gallinarumGQNEI S. typhimuriumGQNEI S. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	Z. mays GGNATY S. gallinarumGQNEI S. typhimuriumGQNEI S. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	P. hybrida GGNSRY Z. mays GGNATY S. gallinarumGQNEI S. typhimuriumGQNEI G. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	h. esculentum GGHSRY h. esculentum GGHSRY P. hybrida GGNSRY Z. mays GGNATY S. gallimarumGQNEI S. typhimuriumGQNEI S. typhiGQNEI E. coliGSNDI K. pneumoniaeGSNDI	N. tabacum GGHSRY L. esculentum GGHSRY L. esculentum GGHSRY P. hybrida GGNSRY Z. mays GGNATY S. gallinarumGQNEI S. typhimuriumGQNEI E. coliGSNDI K. pneumoniaeGSNDI	A. thaliana GGNASY N. tabacum GGHSRY L. esculentum GGHSRY P. hybrida GGNSRY Z. mays GGNATY S. gallinarumGQNEI S. typhimuriumGQNEI E. coliGSNDI K. pneumoniaeGSNDI	B. napus HSGNASY B. napus GGNASY A. thaliana GGNASY N. tabacum GGHSRY L. esculentum GGHSRY P. hybrida GGNSRY Z. mays GGNATY S. gallinarumGQNEI S. typhimuriumGQNEI G. typhi E. coliGSNDI K. pneumoniaeGSNDI	A. nidulans HST.SSQKYI A. nidulans HSSTVDSS B. napus GGNASY A. thaliana GGNASY N. tabacum GGHSRY L. esculentum GGHSRY P. hybrida GGNSRY S. gallimarumGQNEI S. typhimuriumGQNEI S. typhimuriumGQNEI K. pneumoniaeGSNDI	S. cerevisiae NST.SSQKYI A. nidulans HSSTVDSS B. napus GGNASY A. thaliana GGNASY N. tabacum GGHSRY L. esculentum GGHSRY P. hybrida GGNSRY S. gallinarum GGNATY S. typhimurium GGQNEI S. typhimisium GGONEI K. pneumoniaeGSNDI	S. aureus GNES S. cerevisiae NST.SSQKYI A. nidulans HSSTVDSS B. napus GGNASY A. thaliana GGNASY N. tabacum GGHSRY b. esculentum GGHSRY P. hybrida GGNSRY S. gallimarumGQNEI S. typhimuriumGQNEI G. typhi E. coliGSNDI K. pneumoniaeGSNDI	B. subtilis PFYS B. subtilis PFYS S. cerevisiae NST.SSQKYI A. nidulans HSSTVDSS B. napus GGNASY A. thaliana GGNASY N. tabacum GGHSRY I. esculentum GGHSRY P. hybrida GGNSRY S. gallinarumGQNEI S. typhimuriumGQNEI E. coli K. pneumoniaeGSNDI	ILBAA DMKT ISAA DMKT ISGIODACTERIUM CP4 DFYS B. Subtilis PFYS S. GEREVISIAE GNES S. CEREVISIAE NST.SSQKYI A. Nidulans HSSTVDSS B. Napus GGNASY A. thaliana GGNASY I. ESCULENTUM GGNSRY I. ESCULENTUM GGNSRY S. gallimarum GGQNEI S. typhimurium GGQNEI S. typhimurium GGONEI E. coli K. pneumoniaeGSNDI	PG2982 DMKT I.BAA DMLT I.BAA DMKT I.BAA DMKT I.BAA DMKT I.BAA DMLT I.BAA DMKT I.BAA DMLT I.BAA
G	RLSGVPRMHE	MLGGEPRMEE	VIIGHTKMKE	THE TOPPONTE	II.TGFDBMKF	VLTGEPRMKE	VLTGEPRMKE	VLTGEPRMKE	VLTGEPRMKE	VLTGEPRMKE	VLTGEPRMKE	VLDGVPRMRE	VLDGVPRMRE	VLDGVPRMRE										SFIGDASLSK	
RPL	RPIGDLVDAL	RPIGHLVDCL	_	ARILHLVUAL	DDITHIUDAT	RPIGHLVDAI.	RPIGHLVDAL	RPIGHLVDAL	RPIGHLVDSL	RPIGHLVDSL	RPIGHLVDSL	RPIGDLVVGL	RPISDLVDGL	RPIGDLVDGL	RPIGDLVDGL	RPIGDLVVGL	RPIGDLVVGL	RPIGDLVDAL	RPIAPLVDSL	RPMDRVLRPL	RPMKRVTEPL		RPMGRVLNPL	RPMGRVLNPL	
! ! ! ! ! !	RQFGAGIEYL	ALKGAHIQYL	CQAGAEIQYL	KQAGADIRYL	TO TO TO TO TO TO	ROGGAOTDAT	RQGGAQIDYL	RLGGAKITYL	RQGGANIDYL	RQGGANIDYL	RQGGANIDYL	KQLGADVDCF	KQLGAEVDCF	KQLGAEVDCS	KQLGAEVDCF	KQLGADVECT	KQLGADVECT	TANVLPLNTS	RANGTKIEYL	KLMDANIEG.	KKMGAKIDGR	REMGVQVKSE	REMGVQVEAA	REMGVQVEAA	
! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! !	GQAGYPPLRI	KKDGYPPLVV	EQEGYPPIAI	ENEGYPPLAI	EVENIUM.CT	FORMVBB OT	EOENYPPLRL	EQENYPPLRL	EQENYPPLRI	EQENYPPLRL	EQENYPPLRL	LGTDCPPVRV	LGTKCPPVRI	LGTNCPPVRI	LGTNCPPVRI	LGTNCPPVRV	LGTNCPPVRV	KGRASLPLKI	NNEGSLPIKV	IEDNYTPL		DGDRLPVT		DGDRMPL	200

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1 1 1 1 1	1 1 1 1 1 1 1	<u>N</u>	1 1 1 1	; ; ; ; ; ; ; ; ;	Consensus
SGQDITIEVV	LMAAPVLARR	SVSSQFLTAL	GPVRVEG	GGGSIRVD	в. pertussis
. PVI PRIHIK	LMAAPAMA	SVSSQFLTAF	GDVHVDG	DAK.GLWG	A. salmonicida
EADTEIELL	LMAAP.MA	SVSSQFLTAL	GRIQIDG	RNT.GLKG	P. multocida
.ENDTEIEI	LMSAP.LA	SISSQFLTAL	GKVKIDG	RNK.GIKG	H. influenzae
.EQDTEIQIC	LMTAP.LA	SVSSQFLTAL	GKLTVDG	AGGFRG	\subset
. PQDTVIAIK	LMASP.LA	SVSSQFLTAL	GDVEVDG	RGGFTG	$\overline{}$
. PEDTVIRIK	LMTAP.LA	SVSSQFLTAL	GNVDVDG	QGGFTG	E. coli
.PEDTIIRVK	LMTAP.LA	SVSSQFLTAL	GDIEVDG	RGGFIG	
. PKDTIIRVK	LMTAP.LA	SVSSQFLTAL	GDIEVDG	RGGFTG	<u> </u>
. PKDTIIRVK	LMTAP.LA	SVSSQFLTAL	GDIEVDG	RGGFIG	s. gallinarum
.LGDVEIEII	LMAAP.LP	SISSQYLSAL	GKVKLSG	NGIGGLPG	
LGDVEIEII	LMAAP.LA	SISSQYLTAL	GKVKLSG	VSKGGLPG	
.LGDVEIEII	LMAAP.LA	SISSQYLTAL	GKVKLSG	VSKGGLPG	L. esculentum
LGDVEIELL	LMAAP.LA	SISSQYLTAL	GKVKLSG	.VSKGGLPG	N. tabacum
.LGDVEIEIV	LMSAP.LA	SISSQYLTAL	GKVKLSG	NANGGLPG	A. thaliana
.LGDVEIELL	LMAAP.LA	SISSQYLTAL	GKVKLSG	NANGGLPG	
.EPVTLRLVG	LMCAPYAK	KVSSQYVSSL	GNINLAA	AASGGFAG	D
.EPVTLALVG	LMCAPYAE	TVSSQYVSSI	GRIELAA	YTDSVFKG	Œ.
SKETTI	LFASLF	VASAOVKSAI	VIKGINYQME	IIKPS	<u>س</u>
AEGTT	LLAGLQ	VASAQIKSAV	SLKGIDYVSP	SVSGA	B. subtilis
TPGITT	LLAGLN	MASAQVKSAV	TPTPITYRVP	LRGPK	Adrobacterium CP4
TPGVTT	LLAGLN	MASAQVKSAV	TANPITYRVP	LIGPK	LBAA
TPGVTT	LLAGLN	MASAQVKSAV	TANPITYRVP	LIGPK	PG2982
				201	

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Agrobacterium CP4 entuerculitica S. typhimurium salmonicida influenzae pneumoniae gallinarum pertussis multocida esculentum cerevisiae S. typh: S. aureus nidulans subtilis hybrida thäliana E. coli tabacum B. napus 2. mays LBAA

Consensus PG2982 GELISKPYIE GELVSKPYID GEL/VSKPYID GELVSKPYID GEL/VSKPYID GELVSRPYID GDLVSKPYID GELVSKPYID GELVSKPYID GELVSKPYID DKLISIPYVE DKL.ISVPYVE DKLISVPYVE DKLISVPYVE DKLISVPYVE DKLISVPYVE GKPISQPYID GKPISKLYVD VTEPHKSRDH TERMLSAFGV IKELDVSRNH VIEPIMTRDH VIEPVMTRDH TEKMLQGFGA VIEPVMTRDH ITLNLMARFG ITLHIMNSSG ITLKMMQTFG ITLAMMRDFG ITLHLMKAFG ITLHLMKTFG ITLNLMKTFG ITLNLMKTFG MTLRLMERFG ITLNLMKTFG MTLKLMERFG MTLKLMERFG ITLNLMKTFG MTTAMMRSFG MTIKMMEKFG MTLKLMERFG TETMFKHFNI MTLKLMERFG MTLKLMERFG TEKMLQGFGA TEKMLQGFGA VS..V.RRDG VV..IEH.DN VE..VEN.QA VK..VEN.HH VD..VVH.EN VE..VEN.QA VE..IEN.QH VE..IAN.HH VE. VE..IAN.HH VK..AEHSDS VF..VEHSSG IS..VEHSSS VS..VEHTSS VS..VEHSDS VS..AEHSDS ID.. VQKSTJ IN. VET. STT KLSEDQTS. PIEAEGLS. NLTVETDADG DLTVETDKDG DITIVETDKDG .IAN.HH WRAFTIARDA YKLFYIKGNQ YQRFLVKGHQ YQKFQVKGNQ YQIFHIKGGQ YQRFIVRGNQ YQQFVVKGGQ YQQFVVKGGQ YQQFVVKGGQ YQQFVVKGGQ WDRFYIKGGQ WDRFFVRGGQ WDRFLVKGGQ WDKFLVRGGQ WDRFFVKGGQ WDRFFVKGGQ **EEHTYHIPQG** EPYTYYIPKG VRTIRLEGRG VRHIRITGQG VRHIRITGQG ...VSIAGGQ .. INTTPEAI VYRGPGRMAI SIVSPGDFLV QYQSPHRFLV SYISPNKYLV TYRSPGIYLV QYQSPGDYLV SYQSPGTYLV QYHSPGRYLV QYHSPGRYLV QYHSPGRYLV KYKSPKNAYV KYKSPGKAFV KYKSPGKAFV KYKSPGKAYV RYVNPAEYVI HYINPSEYVI KYKSPGNAYV KYKSPGNAYV RYIKPADFHV KLTAA.DIFV KLTGQ.VIDV KLVGQ.TIDV KLVGQ.TIDV

Figure

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К Agrobacterium CP4 entoercolitica salmonicida typhimurium influenzae multoçida pneumoniae gallinarum esculentum pertussis P. hybrida cerevisiae N. tabacum Consensus S. aureus S. typhi nidulans thaliana subtilis B. napus E. coli mays PG2982 LBAA EGDASTASYF EGDASSASYF ESDASCATYP ESDASSATYP PGDISSAAFF PGDISSAAFF FGDPSSTAFP LVAALLVEGS PGDPSSTAFP PGDPSSTAFP D-S----LALGA. IGGG LAAAA.IK.G LAAGA.IK.G LAAGA.IK.G LAAAA.IKGG LAAGA.IKGG LAAAA.IKGG LVAALLVEGS LAAGG.IKGG LAAGA.IKGG LAAGA.IKGG LAGAA.ITGG LAGAA.VTGG LAGAA.VTGG LAGAA.ITGE LAGAA. ITGE LAVAA.VTGT LVAALLVPGS LAGAA. VTGG LAFAA.MTGT IVAALITPGS LAAGAMVPNS PVRVTGVGED TVRVTGIGKQ KVRVTGIGKH KVKVTGVGKN KVKVTGIGKN TVKVTGIGRN TVKVTGIGRN TVKVTGIGGK TVTVEGCGTT TITVEGCGTN TVTVEGCGTS TVKVTGIGRK TVKVTGIGRK T'VT'VEGCGTS TVTVEGCGTT TVTVEGCGTT TCTVPNIGSA RIVLKNVGLN DVTIRNVLMN TVTVPNIGFE DV'TILNVLMN DVTIHNVGIN DVTIRNVLMN SIQGDVAFA. SI.GDIHFA. SIQGDRLFA. SIQGDRLFA SMQGDIRFA SVQGDTKFA SVQGDIRFA SMQGDIRFA SMQGDIRFA SMQGDIRFA SLQGDVKFA SLQGDVKFA SLQGDVKFA SLQGDARFAV SLQGDVKFA SLQGDVKFA SLQGDVKFA SLQGDARFAR OTRSGI... PTRTGL... PTRTGL... PTRTGL... PTRTGI... ATLAAMGADV **DVLERMGARI** DVLEKMGAHI DVLEKMGAKI **DVLEKMGAKI** DVLEKMGATV DVLEKMGATI DVLHKMGATJ DVLEKMGATI DVLEKMGATI EVLEMMGAKV EVLEKMGAEV EVLEKMGAEV EVLEKMGAEV EVLEKMGCKV EVLEKMGCKV EVLRPMGCTV DIVEKMGGNI DVLQNMGAKL LTLQEMGADI DVLKPMGCK LTLQEMGADI LTLQEMGADI ---MG--

Figure

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Consensus	B. pertussis	A. salmonicida	T	-	f. encoercolitica	K. pneumoniae		S. typhi	S. typhimurium	•		P. hybrida		N. tabacum	•		A. nidulāns	ک. CereVisiae		B. SUDCILIS	Agrobacterium CP4	LBAA	PG2982	
; ; ; ; ;	ADG	I.PR	AEG	SNG	ADG	ARG	AKG	AKG	AKG	AKG	A.D.G	ÀDG	ÄDG	ADG	ADG	ADG	HRPMEKSQTT	SHDSDPNSAN	AVG	AEG	AEG	AEG	AEG	101
! ! ! ! !	PCRLRNIGSW	VPPHSQHLQL	ETVIRNIYNW	ETVIRNIYNW	PTVIRNIYNW	TTTLRNIYNW	TTRLRNIYNW	TTTLRNIYNW	TTTLRNIYNW	TTTLRNIYNW	PTAIRDVASW	PTAIRDVASW	PTTIRDVASW	PTAIRDVASW	PTTIRDVASW	PTTIRDVASW	PPVSSGIANQ	TTTIEGIANQ		TTVIKDAAEL	ATVMNGLEEL	ETVMDGLDEL	ETVMDGLDEL	
-VR		AVRD.DRCTP	RVKETDRLTA	RVKETDRLTA	RVKETDRLSA	RVKETDRLFA	RVKETDRLFA	RVKETDRLFA	RVKETDRLFA	RVKETDRLFA	RVKETERMVA	RVKETERMIA	RVKETERMIA	RVKETERMIA	RVKETERMIA	RVKETERMIA	RVKECNRIKA	RVKECNRILA	KVKETNRIDT	KVKETNRIDT	RVKESDRLSA	RVKESDRLAA	RVKESDRLAA	
	MHTELEKLGA	CTHGHRRÃOA	MATELRKVGA	MATELRKVGA	MATELRKVGA	MATELRKVGA	MATELRKVGA	MATELRKVGA	MATELRKVGA	MATELRKVGA	IRTELTKLGA	ICTELRKLGA	ICTELRKLGA	ICTELRKLGA	ICTELRKLGA	ICTELRKLGA	MKDELAKFGV	MATELAKFGV	TADMLNLLGF	VVSELRKLGA	VANGLKLNGV	VARGLEANGV	VARGLEANGV	
	GV.QSGADWL	GVSEEGTTFI	EV.EEGEDFI	EV.EEGEDFI	EV.EEGQDYI	EV.EEGEDYI	EV.EEGHDYI	EV.EEGHDYI	EV.EEGHDYI	EV.EEGHDYI	SV.EEGPDYC	TV.EEGPDYC	TV.VEGSDYC	TV.VEGSDYC	TV.EEGSDYC	TV.EEGSDYC	ICREHDDGLE	KTTELPDGIQ	ELQPTNDGL.I	EIEPTADGMK	DCDEGETSLV	DCTEGEMSLT	DCTEGEMSLT	450

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Consensus	B. pertussis	A. salmonicida	ישי		Y. entoercolitica		E. coli	S. typhi	S. typhimurium	•		P. hybrida		N. tabacum	A. thaliana		A. nidulans	S. cerevisiae		B. subtilis	Agrobacterium CP4	LBAA	PG2982	
:	EVAPPEPGGW	-	-	RIQPLALNQF	RVVPPAQL	RTTPPLTL	RITPPEKL	RITPPAKL	RITPPAKL	RITPPAKL	IITPPEKL	IITPPEKL	IITPPEKL	IITPPEKL	VITPPKKV	VITPPAKV	IDGIDR.SNL	VIIGLNSIKDL	THPSEFKTN.	VYGKQTLKG.	VRGRPDGKGL	VRGRPDGKGL	VRGRPDGKGL	451
1 1 1 1 1 1 1	RDA	RRD	QHA	KHA	IAA	QFA	NFA	QHA	QHA	QHA	NVT	NVT	NVT	NVT	KTA	KPA	RQPVG	KVPSDSSGPV	AT	GA	GNASGA	GGG	GGG	
R-	HIGTWDDHRM	RHLQRSRI	ELNI.HDHRM	NIETYNDHRM	EIGTYNDHRM	EIGTYNDHRM	EIATYNDHRM	DIGTYNDHRM	DIGTYNDHRM	DIGTYNDHRM	AIDTYDDHRM	DIDTYDDHRM	EIUTYDDHRM	EIDTYDDHRM	EIDTYDDHRM	EIDTYDDHRM	GVFCYDDHRV	GVCTYDDHRV	DILTDHRI	AVSSHGDHRI	AVATHLDHRI	TVATHLDHRI	TVATHLDHRI	
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	AMCFLLAAF.	AMCFSLVAL.	AMCFALIAL.	AMCFSLIAL.	AMCFSLVAL.	AMCFSLVAL.	AMCFSLVAL.	AMCFSLVAL.	AMCFSLVAL.	AMCFSLVAL.	AMAFSLAAC.	AMAFSLAAC.	AMAFSLAAC.	AMAFSLAAC.	AMAFSLAAC.	AMAFSLAAC.	AFSFSVL.SL	AMSFSLLAGM	GMMLAVACVL	GMMLGIASCI	AMSFLVMGLV	AMSFLVMGLA	AMSFLVMGLA	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		 				S	s	SS	Ss	S	A	A	A	A	A	A	VTPQ	VNSQNERDEV		T	s	A	A	500

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1 1 1 1 1 1 1				
				Consensus
•		_	PAAVRILDPG (b. pertussis
•	DKI.ASVSOAV	CT'SKTFPDYF I	DIAVTINDPG	ນ 2
AYR	ILFTLNTREV /	CTAKTFPTFL :		_
CLKN	NEFE XI (ייין די אין די אין די אין
•	-	•		H. influenzae
•	FOLARICOTA		D'I'PVTILDPK	· entoercolitica
•	GOLARISTI,A	CTAKTFPDYF (DTPVTILDPK	K. pneumoniae
	EQLARISOAA	CTAKTFPDYF	DTPVTILDPK	
•	EQLARMSTPA	CTAKTFPDYF	D'I'PVTILDPK	S. Cyphi
	EQLARMSTPA	CTAKTFPDYF	DTPVTILDPK	5. CYPhimurium
	EQI,ARMSTPA	CTAKTFPDYF	DTPVTILDPK	
	DVLSTFVKN.	CTRKTFPDYF	EVPVTIRDPG	
•	DVLQQYSKH.	CTRKTFPNYF	DVPVTINDPG	P. nybrida
•	EVI,QKYSKH.	CTRKTFPDYF	DVPVTIKNPG	1. esculentum
•	DVI,QQYSKH.	CTRKTFPNYF	DVPVTIKDPG	
•	QVLERITKH.	CTRKTFPDYF	DVPITINDSG	A. Challana
•	QVLESITKH.	CTRKTFPDYF	DVPVTIKDPG	a. napus
	DTLRQLFKV.	CVGKTWPGWW	PTLILEKE	A. nidulans
	DVLH	CTGKTWPGWW	ANPVRILERH	s. cerevisiae
•	PKLKLLQNEG	AVNVSFPGFL	SEPVKIKQFD	
•	EHLNKLSKKS		EEFLELEHTD	saperits .
ELSDTKA!	DI,MAGLGAKI		ENPVIVUDAT	1:1:44S B
ELSIL	DMMPGLGAKI		ERPVIVDDSN	Action of the Co.
ELSIL	DMMPGLGAKI		EKFVTVDDSN	FG2302
53				FCOGO

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340	AAC AAT CAT CAA TCC CAT CAA CGC TTA ACT GTT AAT CCC CCT GCC CAA
292	GCTTGGTCTT CCCTGCCCCT AATTTTGTCCC CTCC ATG GCC TTG CTT TCC CTC
240	THERCHECCE FGACTAACCG AGGAAAATTE GGCGGGGGC AGAAAEGCCA ATACAATEEA
180	GUGATIUGUUT GTITGAAATIIA ACAAACTGTU GUCCTTUCAU TGACCATGGT AACGATGTTT
120	THE CCATEGG GAATAATGGT ATTITCATTGG TTTGGCCTCT GGTCTGGCAA TGGTTGCTAG
60	AUGUGUTUTA ACUGTAGTAG GGGTCCCGAG CACAAAAGCG GTGCCGGCAA GCAGAACTAA

Asn Asn His Gln 10 Ser His Gln Arg Leu Thr Val Asn Pro 15 Pro 20 Ala Gln

GGG Gly GTC Ala 25 GCTJ'I'G Leu ACT Thr GGC Arg CGC Leu CTA Arg AGG GTG Val CCG GGG Pro Gly Asp 35 GAT Lys AAA Ser TCC Ile ATT 388

Ser His CAT Arg CGG Ala ∙• GCC Leu TTG Met ATG Leu TTG 45 Gly GGG Ala GCG Ile ATC GCC Ala Thr ACC 50 GGG Gly Glu GAA Thr ACC Ile ATT 436

I] e A'I'C GAA Glu Gly GGG Leu Leu CTA CTG nə' J J.,I.,C Gly GGG Glu Asp GAA GAT Pro CCC Arg 65 CGT AGT ACG Ser Thr GCC His CAT Cys TGC

484

Figure 21

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GTC Val	7[5] 999	CTC Leu 135	CT'A Leu	nər]	AT'C Ile	Table The
CAG Gln	GCA Ala	CGT Arg	GCC Ala 120	GAT Asp	GTTP Val	P CGG B Arg
GGT Gly	AAA I.ys	CAC His	GGG Gly	GCG Ala 105	CAG Gln	g GCC
AGC Ser 170	ATT Ile	CGC Arg	CAA Gln	666 61y	GGT Gly 90	ATG Met
CAA Gln	TGG Trp 155	CCC	AAA Lys	AAC Asn	CGG Arg	GGA G1 <i>y</i> 75
T"PA .	GCC Ala	A'TG Met 140	GAT Asp	TCT Ser	GCT Gly	Ala
AAA Lys	CGG Arg	TCC Ser	TGT Cys 125	GGC Gly	CTG Leu	GAA Glu
CCG Pro	AGT Ser	CGG Arg	TTA Leu	ACC Thr 110	GGA Gly	ATC Ile
ATC Ile 175	AAC Asn	GTA Val	TTC Phe	ACC Thr	CAG Gln 95	AGC Ser
CAT His	GGC Gly 160	ATT Ile	ACC Thr	ATG Met	TTG Leu	GAA Glu 80
TAC Tyr	AAG Lys	CAA Gln 145	GTC Val	CGC Arg	CAG Gln	CTA Leu
CAT His	TTT Phe	CCC Pro	ACC Thr 130	TTA Leu	GAA Glu	AAT Asn
TCC Ser	GCG Ala	TTG Leu	GGC Gly	ATG Met 115	CCC	TCA Ser
CCC Pro 180	CCG Pro	CAA Gln	GAT Asp	TTG Leu	AGT Ser 100	GAA Glu
ATT Ile	CTG Leu 165	CAA Gln	GAT Asp	GGC Gly	ACC Thr	AAA Lys 85
GCT Ala	GCA Ala	ATG Met 150	TCC Ser	TTG Leu	GTT Val	ATC Ile
820	772	724	676	628	580	532

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CCC Pro	TCC Ser	GTG Val	CAT His	CGC Arg 215	666 61y	TCA Ser
ACC Thr 280	A'TT Ile	GTG Val	AGC Ser	2 ATG g Met	G GAC Y Asp 200	A GCC r Ala
AGG Arg	TTG Leu 265	CCA Pro	GTC Val	: TTG	ACC Thr	CAG Gln 185
ACA Thr	CCT Pro •	GGG Gly 250	ACT Thr	CAG Gln	ACG	GTA Val
GGG Gly	GGA Gly	GAC Asp	GTC Val 235	GCC Ala	GTT Val	A AAG Lys
G'FG Val	TCA Ser	ATC Ile	CAT His	TrTT Phe 220	' ACA Thr	Ser
TTG Leu 285	GAA Glu	AGC Ser	GGC Gly	GGA Gly	GAA Glu 205	TGC
GAA Glu	TTG Leu 270	TCG Ser	CCG Pro	GCC Ala	CCA Pro	CTG Leu 190
GTG Val	TTG Leu	GCG Ala 255	GCC Ala	AAA Lys	GCT Ala	TTG Leu
TTG	GTG Val	GCC Ala	CAT His 240	TTA Leu	CTA Leu	CTA Leu
GCC Ala	GAA Glu	TT'I Phe	TTA Leu	ACC Thr 225	TCC Ser	GCG Ala
CAG Gln 290	AAT Asn	TGG	ACG Thr	ATT Ile	CGG Arg 210	GGG Gly
ATG Met	GTA Val 275	TTA Leu	GGG Gly	GAT Asp	GAT Asp	TTA Leu 195
GGG Gly	GGC Gly	GTG Val 260	CAA Gln	CCA	CAT His	ACC Thr
GCG Ala	ATT Ile	GCG Ala	CGG Arg 245	GTA Val	AGC Ser	ACC Thr
GAC Asp	AAC Asn	GCA Ala	GTG Val	ACC Thr 230	GAA Glu	GAG Glu
1156	1108	1060	1012	964	916	868

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THACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT ETH PRO Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 310 300 305 310 G CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA 125 210 110 Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Gly Glu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly GGG GGC GAA 125 210 110 Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly GGG GGC GAA 125 210 110 Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly GGG GGC GGC GGC GGC GGC ATT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GAA CTG GGC GCG GCG GGG GGG GGG GGG GGG GGG	GGA G1y	ATG Met 375	GTT Val	GCC Ala	ATT Ile	CTG Leu	ATT T1e 295
C CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 300 G GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA GY Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 325 F CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GAA 225 E Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala GGC GCA GAA CTG GCG GCG GCG Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Glu Leu Arg 345 GCA AGC GAT CGC CTG GCG ATT GAA GAT GCC GCA GAA CTG AGG GGU Ala Ala Ala Ile Ala Ser Glu Leu Arg 355 GAA AGC GAT CGC CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA 365 GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAG ATT CAA GGG AAA 11 Leu Gly Lys 385 GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG AAA 380 GCC AAA GTA CAA CAA GAG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC TTG ACG GAT CAT CGC GAG TTG ACG GAT CAT CGC GAG GTG GAT CAT CGC GAG GTG GAT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC GAG GTG AAB ATT CAA GGG ATT CAT CGC ATT CAT CAT CGC ATT CAT CGC ATT CAT CGC ATT CAT CAT CAT CAT CAT CAT CAT CAT CA	AGC Ser	Gly					
GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT GIL ASN GILL ARG LEU VAI THR GIY GILL PRO VAI ALA ASP 300 AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA ARG ALA SER HIS LEU GIN GIY CYS THR PHE GIY GIY GILL AND 325 CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCA ARG LEU IIE ASP GILL IIE PRO IIE LEU ALA ALA ALA GILL CTG ACG TTC GGC GCA GAA ALA ALA GILL GLU AND ALA ALA GILL CTG GCG ATT GAA GAT TCG GCA GAA CTG AGG GILL GLU AND ALA ALA GILL ALA ALA GILL CHA AND ALA SER GILL GLU AND ALA GILL CHA AND ALA GILL CHA AND ALA GILL CHA AND ALA GILL CHA AND AND ALA GILL CHA GGG LYS AAAA GILL ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG LYS AAAA GILL ACC GAA TTT GAT GAT GGC TTG GAA ATT CAA GGG LYS AAAA GILL ACC GAA TTT GAT GAT GGC TTG ACG GAT CAT CGC CHU GLU GLU ALA AND AND ALA GLU GLU GLU AND AND ALA GLU GLU AND AND ALA GLU GLU ALA AND AND ALA GLU GLU AND	CCG Pro	GCC Ala			E. Pro		
3 AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT ASN GIU ARG Leu Val Thr Gly Glu Pro Val Ala Asp 300 305 306 306 307 308 308 309 309 300 300 307 308 308 308 309 309 309 309 309 309 309 309 309 309	T'T'A I.eu		AGC Ser				
The GAA CGA TTTG GTA ACG GGG GAA CCG GTA GCA GAT GILL ARE LEU Val Thr Gly Glu Pro Val Ala Asp 300 305 310 A AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA SER His Leu Gln Gly Cys Thr Phe Gly Gly Glu 325 ACT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG GAA ATT CCC ATT GTG GCA GTG GCG GCG Thr Thr Are Ile Glu Asp Ala Glu Leu Arg 350 355 ACC CTG GCG ATT GAA GAT GCC GCA GAA CTG AGG THr Glu Ala Ala Ile Ala Ser Glu Leu Gly Lys 365 ACC GAA TTT GAT GAT GCC CTG GAG TTG GCC AAA ATT GLU Ala Ala Ile Ala Ser Glu Leu Gly Lys 365 ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG THr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 380 GCG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC GTY Ala GIU Val Asp Ser Leu Thr Asp His Arg 405	CAA Gln 395	GTC Val					
A CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT u Arg Leu Val Thr Gly Glu Pro Val Ala Asp 305 C CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA r His Leu Gln Gly Cys Thr Phe Gly Gly Glu 320 P GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG ASP Glu Ile Pro Ile Leu Ala Val Ala Ala 335 ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 350 CTG GCG GCC ATT GAT GCT TCG GAG TTG GGC AAA Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 365 GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 385 GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Ala Glu Val Asp Ser Leu Thr Asp His Arg 400	GGG G1y	ACC Thr 380	Arg				
A TTG GTA ACG GGG GAA CCG GTA GCA GAT GLEU VAL Thr Gly Glu Pro Val Ala Asp 305 T CTC CAG GGT TGC ACC TTC GGC GGC GAA SE Leu Gln Gly Cys Thr Phe Gly Gly Glu 325 F GAA ATT CCC ATT TTG GCA GTG GCG GCG GCG GGU Ile Pro Ile Leu Ala Val Ala Ala Ala Ala Sp 335 CGC ATT GAA GAT GCC GCA GAA CTG AGG ATG Ile Glu Asp Ala Ala Glu Leu Arg 350 GCG GCC ATT GCT TCG GAG TTG GGC AAA Ala Ala Ile Ala Ser Glu Leu Gly Lys 370 TTT GAT GAT GGC CTG GAA ATT CAA GGG Phe Asp Asp Gly Leu Glu Ile Gln Gly 385 GAG GTG GAT AGC TTG ACG GAT CAT CGC Glu Val Asp Ser Leu Thr Asp His Arg 405					l' GA' e Ası		
G GTA ACG GGG GAA CCG GTA GCA GAT u Val Thr Gly Glu Pro Val Ala Asp 305 C CAG GGT TGC ACC TTC GGC GGC GAA 1 Gln Gly Cys Thr Phe Gly Gly Glu 320 A ATT CCC ATT TTG GCA GTG GCG GCG 1 Ile Pro Ile Leu Ala Val Ala Ala 335 ATT GAA GAT GCC GCA GAA CTG AGG 11e Glu Asp Ala Ala Glu Leu Arg 355 GCC ATT TCG GAG TTG GGC AAA Ala Ile Ala Ser Glu Leu Gly Lys 370 GAT GAT GGC CTG GAA ATT CAA GGG Asp Asp Gly Leu Glu Ile Gln Gly 385 GTG GAT AGC TTG ACG GAT CAT CGC Val Asp Ser Leu Thr Asp His Arg 400							
ACG GGG GAA CCG GTA GCA GAT Thr Gly Glu Pro Val Ala Asp 305 GGT TGC ACC TTC GGC GGC GAA Gly Cys Thr Phe Gly Gly Glu 320 CCC ATT TTG GCA GTG GCG GCG Pro Ile Leu Ala Val Ala Ala Glu Asp Ala Ala Glu Leu Arg Glu Asp Ala Ala Glu Leu Arg 370 GAA GAT GCC TCG GAG TTG GGC AAA Ile Ala Ser Glu Leu Gly Lys 370 GAT GGC CTG GAA ATT CAA GGG ASP Gly Leu Glu Ile Gln Gly 385 ATT AGC TTG ACG GAT CAT CGC 11	GTG Val	GAT Asp					G GT u Va
GGG GAA CCG GTA GCA GAT CGly Glu Pro Val Ala Asp 305 TGC ACC TTC GGC GGC GAA CYS Thr Phe Gly Gly Glu ATT TTG GCA GTG GCG GCG Ile Leu Ala Val Ala Ala Asp Asp Ala Ala Glu Leu Arg GCT TCG GAG TTG GGC AAA Ala Ser Glu Leu Gly Lys 385 GGC TTG ACG GAT CAT CGC Ser Leu Thr Asp His Arg 405	GAT Asp 400						
GAA CCG GTA GCA GAT Glu Pro Val Ala Asp 310 ACC TTC GGC GGC GAA Thr Phe Gly Gly Glu 325 'TTG GCA GTG GCG GCG Leu Ala Val Ala Ala 340 GCC GCA GAA CTG AGG Ala Ala Glu Leu Arg 355 TCG GAG TTG GGC AAA Ser Glu Leu Gly Lys 370 CTG GAA ATT CAA GGG Leu Glu Ile Gln Gly 390 TTG ACG GAT CAT CGC Leu Thr Asp His Arg 405	AGC Ser	GGC G1y 385					
A CCG GTA GCA GAT I Pro Val Ala Asp 310 TTC GGC GGC GAA C Phe Gly Gly Glu 325 GCA GTG GCG GCG Ala Val Ala Ala 340 GCA GAA CTG AGG Ala Glu Leu Arg 355 GAA ATT CAA GGG Glu Ile Gln Gly 390 ACG GAT CAT CGC Thr Asp His Arg 405	TTG Leu	CTG Leu					
GTA GCA GAT Val Ala Asp 310 GGC GGC GAA Gly Gly Glu 325 GTG GCG GCG Val Ala Ala 340 GAA CTG AGG Glu Leu Arg TTG GGC AAA Leu Gly Lys ATT CAA GGG Ile Gln Gly 390 GAT CAT CGC Asp His Arg 405	ACG Thr	GAA Glu					
A GCA GAT 1 Ala Asp 310 2 GGC GAA 2 Gly Glu 325 3 GCG GCG Ala Ala CTG AGG Leu Arg GGV Lys GAA GGG Gly Lys CAA GGG Gln Gly 390 CAT CGC His Arg 405	GAT Asp	ATT Ile					
A GAT A ASP 310 GAA GGCG AGG ARG AAA Lys GGLy 390 CGC Arg	CAT His 405	CAA Gln					
	CGC Arg	GGG Gly 390					
1204 1252 1300 1348 1348 1344			·	- u	U)	, , , , , , , , , , , , , , , , , , ,	O O
	1492	1444	1396	1348	1300	1252	1204

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1894	CCACTTATAA CTTPCGGGA
1875	GAGTAGAAGT AATGGGGCCCA AACGGCGATC GCCACGGGAA ATTAAAGCCT GCATCACTGA
1815	TUUUTTIPAAT TUUTTAAAAG UTOGUTTAAA ACTGUUAAC GTATUTUUGT AATGGUGAGT
1755	GGGTAATTTA TCCGCAATTG ACCAATCGGC ATGGACCGTA TCGTTCAAAC TGGGTAATTC
1695	GGCGGTTTTGT AAATGTTTTA CCAAGGTAGT TTGGGGTAAA GGCCCCAGCA AGTGCTGCCA
1635	GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG Gly Thr Leu Gly Gln Val Ala Gln Gly 440
1588	ATT AAC CGG GCG GAA GCG GCC GCC ATT TCC TAT CCA GAA TTT TTT Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe 425
1540	ATT GOO ATG GOO TOO GOO ATC GOO GOT TTA GOT AGT GGG GGG CAA ACA Ile Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr 410

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TTA Leu 180	TTA Leu	GCG Ala	CCG Pro	TGC	CGT Arg 100	CAG Gln
TTG	CCG Pro 165	CCG Pro	CTT Leu	Gly	r TrA J Leu	3 CCG n Pro 85
GCT Ala	CTT Leu	TTA Leu 150	GTG Val	GAT' Asp	TTG Leu	CCG
GAC Asp	CCC AGC Pro Ser	CAT His	CAA Gln 135	GAA Glu	GCA Ala	AAA Lys
GGT Gly		ATT' Ile	ATG Met	TCA Ser 120	. GGA . Gly	GCA Ala
ACC Thr 185	GCG Ala	TCA Ser	с66 61у	'I"l'A Leu	A'l'T Ile 105	CCG
ACG Thr	CAA Gln 170	GGA Gly	GCA Ala	GAA Glu	TTG	TTA Leu 90
CGG Arg	TTA Leu	CGC Arg 155	AAA Lys	AAA Lys	GCA Ala	AAT Asn
CTG (Leu]	AAA Lys	CCG Pro	ATT Ile 140	CGT Arg	GCG Ala	ATG Met
CAT .	AGT Ser	CTG Leu	GTC Val	CCG Pro 125	CAG Gln	CAA Gln
ACT Thr (TGC Cys	ACC	AGT Ser	ATG Met	CGC Arg 110	AAC Asn
TGC Cys (CTT Leu 175	GGC Gly	CAC His	CAG Gln	TTT Phe	AGT Ser 95
GGC Gly	ATT Ile	ATT Ile 160	AGC Ser	CGC Arg	GAG Glu	GGC Gly
ATC Ile	TTG Leu	GAT Asp	AAT Asn 145	ATT Ile	AGC Ser	ACT Thr
AGT Ser	GCA Ala	TAC Tyr	TTT Phe	ATT Ile 130	GTG Val	AGC Ser
CGC Arg 195	GGA Gly	GCG Ala	ACG Thr	ACG Thr	TTA Leu 115	ATG Met
691	643	595	547	499	451	403

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GCA Ala	GGA Gly	A1TI 11e 260	GCG Ala	GTG Val	AAG Lys	GAC Asp
GAT Asp	CGG Arg	AAT Asn	GCT Ala 245	3 CTT	G AAA s Lys	C CAC p His
ATT Ile	ATTI Ile	Pro	r Tro	T GAT	A GAG s Glu	oc Acc s Thr
GTT Val 295		ACG Thr	3 ATT 1 Ile	T ATT p Ile 0	G CAA u Gln 215	CG GAA nr Glu
GTT Val	GAA TTG Glu, Leu 280	G CGG	T GCG e Ala	'n GTC e Val	A ATA n 11e 5	
TAT Tyr	G CAT	3 GCG g Ala 265	G CCG a Pro	rc GGC		
CAT	r CAT				ATC (ATG '
		GCA . Ala	CGC Arg 250	GAT Asp	GTC Val	TTG Leu
TCA . Ser !	CAG Gln	ATC Ile	GCG Ala	TTG Leu 235	ACC Thr	CCG Pro
AAA Lys 300	CGC Arg	ATT Ile	GAA Glu	TCG Ser	GGT Gly 220	CTT
TTG Leu	TTT Phe 285	ACT Thr	GTC Val	GCG Ala	GGA Gly	TTT Phe
CGC Arg	TGG	TTG Leu 270	GTT Val	GCG Ala	CAA Gln	GGT Gly
GGC Gly	GGC Gly	ner] Ten	ATT Ile 255	GCG Ala	AAA Lys	GGC
ATT Ile	GCC Ala	CAA Gln	CGT Arg	TTT Phe 240	TTG Leu	GCA Ala
ACG Thr 305	GAA Glu	AAA Lys	AAT Asn	TTT Phe	CAC His 225	CTT
GTG Val	CCG Pro 290	ATG Met	GTC Val	ATG Met	GGT Gly	GAG Glu 210
GCG Ala	GTG Val	GGC G1y 275	GGC Gly	GTT Val	TGC Cys	ATC Ile
1027	979	931	883	835	787	739

GCA Ala	GGC G1y	TAT Tyr	CAA Gln	TTG Leu 340	GCG Ala	CCG Pro
GGT Gly 405	GAT Asp	GGA Gly	ACT Thr	G CGT 1 Arg	G GCA a Ala 325	G GAA
GAA Glu	CAT His 390	AGA Arg	r TTG r Leu	T GTG g Val	CA GCT a Ala 5	
TTA Leu	Arg	A AGC J Ser 375	G GGC u Gly	G AAA 1 Lys		Trp I
TTG Leu	ATT	C GAT r Asp	C GTG Y Val 360	AA GAA 's Glu		ATT G Ile A
A'TT Ile	f GCG e Ala	T CGG P Arg			GCG G Ala G	GCC ! Ala !
			GCG Ala	11'CG Ser 345	GAA Glu	AAC Asn
GAT (Asp / 410	ATG . Met	CAA Gln	TGC Cys	GAT Asp	GGG Gly 330	GCG Ala
GAC Asp	AGT Ser 395	TTT Phe	GAC Asp	<u>CGT</u> Arg	ACG Thr	ATT Ile 315
GGC Gly	TTG Leu	TTA Leu 380	GTT Val	TTA	ACT	F GAT B Asp
GCG Ala	GCG Ala	CCG Pro	GGC G1y 365	GCG Ala	r TTT	r GAA o Glu
GTG Val	GTG Val	GCG Ala	GCC Ala	GCG Ala 350	r GTG e Val	A TTG
GCG Ala 415	GCA Ala	CGG Arg	GAT Asp	ATG Met	335	G CCG
GCG Ala	GGT Gly 400	GTG Val	TTT	GCG Ala	AAT Asn	ATT Tile 320
GTT Val	GTG Val	AAC Asn 385	ATT Ile	CAA Gln	f TTG	r TTT e Phe
TCT Ser	CGC Arg	AGT Ser	CAT His 370	AAT Asn	TCA Ser	r TTT
ATG Met	GCG Ala	TTT Phe	ATA Ile	TTA Leu 355	GAA Glu	ATT
		-			سر <u>۔</u>	בי עו
1363	1315	1267	1219	1171	1123	1075

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CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA Pro Gln Phe Arg Asp Phe Ala Ala Ile Gly Met Asn Val Gly Glu 420 435

Lys Asp Ala Lys Asn Cys His Asp AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTTG GAAAAGGCAC 440 1465

GGTGGCGCAA GCTT

1479

Figure 22

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Consensus	•	\Box	B. s	Synechocystis sp. PCC6803	Agrobacterium CP4	LBAA	PG2982		Consensus	S. aureus	D. nodosus		Synechocystis sp. PCC6803	Agrobacterium CP4	LBAA	PG2982		Consensus	S. aureus	D.	ω,	synechocystis sp. PCC6803	7 P A		
T		TRLHTCGISR DHTERMLPLF	TTVTEPHKSR DHTERMLSAF	TTVTEPALSR DHSERMLQAF	TTVIEPIMTR DHTEKMLQGF	TTVIEPVMTR DHTEKMLQGF	TTVIEPVMTR DHTEKMLQGF	201		YTPLIIKPS VIKGINYQME	T.APLHISGR PLTGIDYALP	•	KFAPLAVQGS QLKPIHYHSP		RMPLTLIGPK TANPITYRVP	RMPLTLIGPK TANPITYRVP	161	GD-SRPM	GLGN.ESVLS GDVSIGKRPM		G.RPFYSAVA GDESIAKRPM	-	VY.DFDSTFI GDASLTKRPM	TY.DMKTSFI GDASLSKRPM	
	INTT	GGALE IKKEQI						0.8.7	SAU-NSLA-L	VKSAL L		IKSAV L					200	-RVPLM1	PLKLM DANIE	_	PLKKM	PLQQM	PLREM	GRVLNELREM GVQVEAADGD	160

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PG2982 LBAA Agrobacterium CP4 Synechocystis sp. PCC6803 * B. subtilis b. nodosus S. aureus Consensus	PG2982 LBAA Agrobacterium CP4 Symechocystis sp. PCC6803 B. subtilis D. nodosus S. aureus Consensus	PG2982 LBAA Agrobacterium CP4 Synechocystis sp. PCC6803 B. subtilis D. nodosus S. aureus Consensus
VR.ASKLKGV VVPPERAPSM VR.ASKLKGV VVPPERAPSM VR.SSTLKGV TVPEDRAPSM VR.ASHLQGC TFGGEIIPRL IE.TSSLKAV EIGGDIIPRL VY.HSKLRGI TVAPEWIANA IQYTPMLQPI TIEGELVPKA VLE	LMNPTRT GLILTLQEMG LMNPTRT GLILTLQEMG LMNPTRT GLILTLQEMG GINPTRT GVLEVLAQMG GLNPTRT GIIDVLQNMG GINPTRA AIITLLQKMG GINQTRS GIIDIVEKMG GINQTRS GIIDIVEKMG	IRITGQGKLV GQTIDVPGDP IRITGQGKLV GQTIDVPGDP IRLEGRGKLT GQVIDVPGDP .TVHGPAHLT GQRVVVPGDI .SIAGGQKLT AADIFVPGDI .IVTGGQKLH GCVLDIVGDL IKPADFHVPGDI
IDEYPVLAIA IDEYPVLAIA IDEYPILAVA IDEIPIIALL IDELPIFFIA IDELPVIALL IDELPVIALL	ADIEVLNARL ADIEVINPRL ADIEVINPRL ADITPENERL ADITPENERL AKLEIKPSAD GRIELHHQRF GNIQLFNQT.	SSTAFPLVAA SSTAFPLVAA SSTAFPLVAA SSAAFWLVAA SSAAFFLAAG SAAAFFMVAA SSAAFFIVAA SSAAFFIVAA
360 ASFAEGETVM ASFAEGETVM AAFAEGATVM AAFAEGTTRI ATQAEGTTVI AACAEGTTFV CTQAVGTSTIA-G	320 AGGEDVADLR AGGEDVADLR AGGEDVADLR VTGEPVADLR SGAEPYGDLI WGAEPVADIV TGAEPTASIR	LLVEGSDVTI LLVEGSDVTI LLVEGSDVTI LLVPGSDVTI SILPGSELLV AMVPNSRIVL LIAPRAEVVI LITPGSDVTI

23

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	COnsensus	o. aureus		ני אחטרדודא	•	Synechocystic of Toccord	Agrobactori Gal	F62382			Consensus	S. aureus	D. nodosus	B. subtilis	Synechocystis sp. PCC6803	Agrobacterium CP4	LBAA	PG2982	
441		EFK TNATDILTDH	SURQFL PARVNSFGDH		SPLQ GAEVDSLTDH	PUGKGLGNAS GAAVATHLDH	PDGKGLG GGTVATHLDH	PUGKGLG GGTVATHLDH RIAMSFLVMG	# O L	401	EL-VKER	KDAEELKVKE TNRIDTTADM	GNLSELRVKE SDRLAAMAQN	KDAAELKVKE TNRIDTVVSE	EDAAELRVKE SDRLAAIASE	NGLEELRVKE SDRLSAVANG	DGLDELRVKE SDRLAAVARG	DGLDELRVKE SDRLAAVARG	361
173	L-V	LAVAC	RIAMSLAVAG VRAAGELLID	RIGMMLGIAS CITEEPIEIE	RIAMALAIAA LGSGGQTIIN	RIAMSFLVMG LVSENPVTVD	RIAMSFLVMG LAAEKPVTVD	RIAMSFLVMG LAAEKPVTVD	440		LG	LNLLGFELOP	LQTLGVACDV	LRKLGAEIEP	LGKMGAKVTE	LKLNGVDCDE	LEANGVDCTE	LEANGVDCTE GEMSITV	400

Consensus

----P

-F-----

AKIELSIL..

AKIELSIL..

AKIELSDTKA

QG*.....

KKS......

MNVGEKDAKN

NEG.....

CHD

QFDAVNVSFP GFLPKLKLLQ

Synechocystis sp. PCC6803

subtilis nodosus aureus

HTDAIHVSYP

DATMIATSFP RAEAAAISYP

EFFGTLGQVA

DGAVAAVSMP

QFRDFAAAIG

TFFEHLNKLS

Agrobacterium CP4

PG2982

LBAA

DSNMIATSFP EFMDMMPGLG

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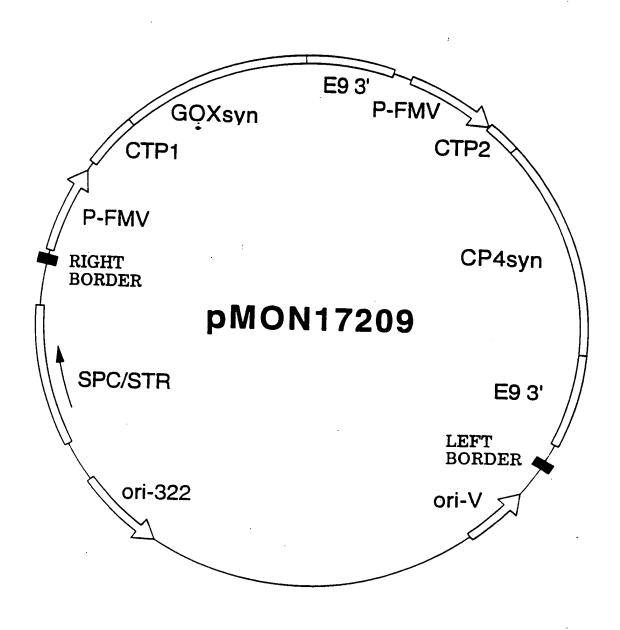


Figure 24

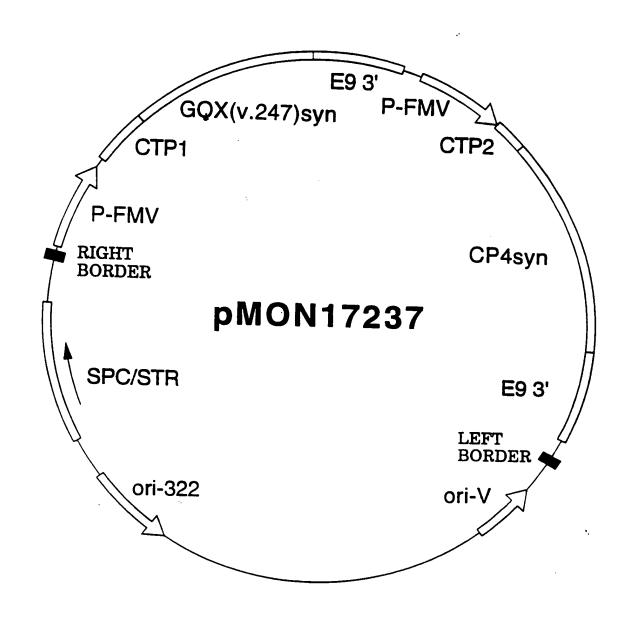


Figure 25